

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 24, 2005, 18:26:36 ; Search time 2360 Seconds
(without alignments)
15349.114 Million cell updates/sec

Title: US-10-063-553-47
Perfect score: 766
Sequence: 1 ggctcgagcgttctgagc.....agtagtttgaaaaaaa 766

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : GenEmbl:

- 1: gb_ba:*
- 2: gb_htg:*
- 3: gb_in:*
- 4: gb_om:*
- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pl:*
- 9: gb_pr:*
- 10: gb_ro:*
- 11: gb_sts:*
- 12: gb_sy:*
- 13: gb_un:*
- 14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	766	100.0	766	6	AR252552 Sequence
2	766	100.0	766	6	AX092316 Sequence
3	766	100.0	766	6	AX376130 Sequence
4	766	100.0	766	6	AX403370 Sequence
5	766	100.0	766	9	AY358671 Homo sapi
6	747	97.5	2308	9	AK026453 Homo sapi
7	332	43.3	46778	2	AC079784 Homo sapi
8	332	43.3	206624	9	AC097662 Homo sapi
9	264.2	34.5	351	6	AX246020 Sequence
10	231.4	30.2	286	6	AX098190 Sequence
11	184	24.0	201	6	CQ741848 Sequence
12	171.6	22.4	203478	10	AC138214 Mus muscu
13	168.2	22.0	209326	2	AC106407 Rattus no
14	168.2	22.0	257693	2	AC103323 Rattus no
15	148.6	19.4	378	6	AX246229 Sequence
16	128.8	16.8	208731	2	AC129037 Rattus no
17	92.8	12.1	308833	2	AC106408 Rattus no
18	60	7.8	60	6	CQ550697 Sequence
19	50.2	6.6	873	5	BX932079 Gallus ga

C	20	49.2	6.4	110000	2	AC112083_1	Continuation (2 of
C	21	48.6	6.3	853	5	BX935444	BX935444 Gallus ga
C	22	46.2	6.0	137088	9	AC135628	AC135628 Homo sapi
C	23	45	5.9	132384	9	AC116347	AC116347 Homo sapi
C	24	45	5.9	168242	9	AC140830	AC140830 Homo sapi
C	25	45	5.9	168430	2	AC145037	AC145037 Homo sapi
C	26	45	5.9	173275	2	AC145031	AC145031 Homo sapi
C	27	45	5.9	175559	2	AC145101	AC145101 Homo sapi
C	28	43.8	5.7	1141	6	AX083744	AX083744 Sequence
C	29	43.4	5.7	2000	6	AX655393	AX655393 Sequence
C	30	42.4	5.5	181307	5	BX649358	BX649358 Zebrafish
C	31	41	5.4	190499	2	AC068392	AC068392 Homo sapi
C	32	41	5.4	190845	9	AC108695	AC108695 Homo sapi
C	33	40.8	5.3	146479	9	AC097472	AC097472 Homo sapi
C	34	40.8	5.3	191081	2	AC023143	AC023143 Homo sapi
C	35	40.4	5.3	87394	9	HSJ718D20	AL121830 Human DNA
C	36	40.4	5.3	149310	2	AC148196	AC148196 Callithri
C	37	40.2	5.2	107593	2	AC107484	AC107484 Homo sapi
C	38	40.2	5.2	167791	9	AC108075	AC108075 Homo sapi
C	39	39.8	5.2	189968	9	AC007682	AC007682 Homo sapi
C	40	39.6	5.2	263405	2	AC124845	AC124845 Rattus no
C	41	39.6	5.2	268894	2	AC129448	AC129448 Rattus no
C	42	39.4	5.1	8031	6	CQ719320	CQ719320 Sequence
C	43	39.4	5.1	8034	9	HSY16241	Y16241 Homo sapien
C	44	39.2	5.1	1577	9	AK098573	AK098573 Homo sapi
C	45	39.2	5.1	72000	9	AP002958	AP002958 Homo sapi
C	46	39.2	5.1	153733	2	AC011980	AC011980 Homo sapi
C	47	39.2	5.1	159946	2	AC079194	AC079194 Homo sapi
C	48	39.2	5.1	172848	2	AP001532	AP001532 Homo sapi
C	49	39.2	5.1	176680	9	AC090358	AC090358 Homo sapi
C	50	39.2	5.1	178182	2	AP001400	AP001400 Homo sapi
C	51	39.2	5.1	219382	5	BX247881	BX247881 Zebrafish
C	52	39	5.1	193593	2	BX927289	BX927289 Danio rer
C	53	38.8	5.1	185141	2	AC150601	AC150601 Callithri
C	54	38.8	5.1	349980	6	AX344563	AX344563 Sequence
C	55	38.6	5.0	150578	2	AC135551	AC135551 Sus scrof
C	56	38.6	5.0	155376	9	AC027026	AC027026 Homo sapi
C	57	38.6	5.0	231113	2	AC094980	AC094980 Rattus no
C	58	38.6	5.0	241062	2	AC113725	AC113725 Rattus no
C	59	38.2	5.0	849	1	AF405549	AF405549 Helicobac
C	60	38.2	5.0	7218	6	I66494	I66494 Sequence 14
C	61	38.2	5.0	89712	2	AC021459	AC021459 Homo sapi
C	62	38.2	5.0	171627	2	AC117776	AC117776 Mus muscu
C	63	38.2	5.0	192885	2	AC117732	AC117732 Mus muscu
C	64	38.2	5.0	195499	2	AC092257	AC092257 Mus muscu
C	65	38.2	5.0	243990	2	AC092260	AC092260 Mus muscu
C	66	38.2	5.0	258805	2	AC113467	AC113467 Mus muscu
C	67	38	5.0	185143	2	AC025861	AC025861 Homo sapi
C	68	38	5.0	216636	2	AC112069	AC112069 Rattus no
C	69	38	5.0	244687	2	AC095483	AC095483 Rattus no
C	70	37.8	4.9	151900	9	AC107419	AC107419 Homo sapi
C	71	37.8	4.9	154594	9	AL161722	AL161722 Human DNA
C	72	37.8	4.9	167395	9	AC055858	AC055858 Homo sapi
C	73	37.8	4.9	169742	10	AL646101	AL646101 Mouse DNA
C	74	37.8	4.9	214702	9	AC020689	AC020689 Homo sapi
C	75	37.8	4.9	226119	2	AC099445	AC099445 Rattus no
C	76	37.8	4.9	228414	2	AC128563	AC128563 Rattus no
C	77	37.8	4.9	231998	2	AC113222	AC113222 Homo sapi
C	78	37.6	4.9	104296	8	CNS08C8H	AL731877 Oryza sat
C	79	37.6	4.9	128945	9	AL449083	AL449083 Human DNA
C	80	37.6	4.9	138586	8	AC144726	AC144726 Medicago
C	81	37.6	4.9	157677	2	AP002470	AP002470 Homo sapi
C	82	37.6	4.9	162646	9	AC078809	AC078809 Homo sapi
C	83	37.6	4.9	241783	2	AC106100	AC106100 Rattus no
C	84	37.6	4.9	244861	2	AC106089	AC106089 Rattus no
C	85	37.4	4.9	39991	9	AC125815	AC125815 Homo sapi
C	86	37.4	4.9	54255	8	AP003608	AP003608 Oryza sat
C	87	37.4	4.9	110000	1	CR543861_23	Continuation (24 o
C	88	37.4	4.9	115768	2	AP000712	AP000712 Homo sapi
C	89	37.4	4.9	119300	9	AC125766	AC125766 Homo sapi
C	90	37.4	4.9	165990	2	AC093287	AC093287 Homo sapi
C	91	37.4	4.9	172697	9	AC055782	AC055782 Homo sapi
C	92	37.4	4.9	174616	10	AC109307	AC109307 Mus muscu

93	37.4	4.9	181568	2	AC122124	AC122124 Mus muscu
94	37.4	4.9	182816	5	AC145913	AC145913 Gallus ga
95	37.4	4.9	187131	2	AP001535	AP001535 Homo sapi
96	37.4	4.9	187332	9	AC053544	AC053544 Homo sapi
C 97	37.4	4.9	205059	10	AC121778	AC121778 Mus muscu
C 98	37.4	4.9	214795	2	AP001122	AP001122 Rattus no
99	37.4	4.9	217393	9	AP001122	AP001122 Homo sapi
100	37.2	4.9	217393	5	AF287485	AF287485 Oncorhync
101	37.2	4.9	112484	10	AL954640	AL954640 Mouse DNA
C 102	37.2	4.9	127653	8	AC135316	AC135316 Medicago
103	37.2	4.9	129108	9	AC011482	AC011482 Homo sapi
104	37.2	4.9	147890	10	BX936292	BX936292 Mouse DNA
C 105	37.2	4.9	151950	2	AC084813	AC084813 Homo sapi
C 106	37.2	4.9	162525	5	BX004981	BX004981 Zebrafish
107	37.2	4.9	171061	2	BX950177	BX950177 Danio rer
108	37.2	4.9	176010	5	AL935062	AL935062 Zebrafish
109	37.2	4.9	180106	10	AL731676	AL731676 Mouse DNA
C 110	37.2	4.9	181532	2	AC020700	AC020700 Homo sapi
111	37.2	4.9	184213	9	AC073539	AC073539 Homo sapi
112	37.2	4.9	195634	2	AC150472	AC150472 Papio anu
C 113	37.2	4.9	209567	2	AC148249	AC148249 Ootlemur
C 114	37	4.8	92320	9	AC024246	AC024246 Homo sapi
115	37	4.8	150181	5	BX248087	BX248087 Zebrafish
116	37	4.8	157450	2	AC150735	AC150735 Papio anu
C 117	37	4.8	185470	9	AC010947	AC010947 Homo sapi
118	37	4.8	194257	5	BX255948	BX255948 Zebrafish
C 119	37	4.8	231919	2	AC111770	AC111770 Rattus no
120	37	4.8	347050	3	PFA929351	AL929351 Plasmodiu
121	36.8	4.8	12540	1	AE008523	AE008523 Streptoco
C 122	36.8	4.8	122543	9	AC012470	AC012470 Homo sapi
C 123	36.8	4.8	124018	2	AC149732	AC149732 Bos tauru
C 124	36.8	4.8	128561	2	AC068729	AC068729 Homo sapi
125	36.8	4.8	161661	2	AC119283	AC119283 Mus muscu
C 126	36.8	4.8	166120	9	AC073588	AC073588 Homo sapi
C 127	36.8	4.8	184989	10	AC131652	AC131652 Mus muscu
128	36.8	4.8	199896	2	AC127812	AC127812 Rattus no
129	36.8	4.8	219283	2	AC108550	AC108550 Rattus no
C 130	36.8	4.8	231373	2	AC112543	AC112543 Rattus no
C 131	36.8	4.8	252614	5	BX255907	BX255907 Zebrafish
C 132	36.6	4.8	2755	14	AF014881	AF014881 Holliyhock
C 133	36.6	4.8	37425	3	U80842	U80842 Caenorhabdi
134	36.6	4.8	99799	9	AL445184	AL445184 Human DNA
135	36.6	4.8	116380	9	HS688G8	AL031671 Human DNA
C 136	36.6	4.8	132688	2	AC119878	AC119878 Mus muscu
C 137	36.6	4.8	133974	2	AC108894	AC108894 Bos tauru
138	36.6	4.8	135209	9	HS42616	AL020997 Human DNA
139	36.6	4.8	149176	10	AC132097	AC132097 Mus muscu
C 140	36.6	4.8	150553	2	AC127261	AC127261 Mus muscu
C 141	36.6	4.8	150594	2	AC108889	AC108889 Bos tauru
142	36.6	4.8	156223	10	AC119615	AC119615 Rattus no
143	36.6	4.8	166294	2	AC122113	AC122113 Atelerix
144	36.6	4.8	183856	2	AC021300	AC021300 Homo sapi
145	36.6	4.8	193094	2	AC136129	AC136129 Rattus no
C 146	36.6	4.8	202792	9	CNS06C83	AL391158 Human chr
C 147	36.6	4.8	241948	2	AC115203	AC115203 Rattus no
C 148	36.6	4.8	257118	2	AC108341	AC108341 Rattus no
149	36.6	4.8	289087	2	AC110678	AC110678 Rattus no
C 150	36.4	4.8	369	6	AR348554	AR348554 Sequence
C 151	36.4	4.8	2145	3	DDISAS1A	M34456 Dictyosteli
152	36.4	4.8	41483	3	U80023	U80023 Caenorhabdi
153	36.4	4.8	84632	9	AL450026	AL450026 Human DNA
154	36.4	4.8	100000	9	AP000070	AP000070 Homo sapi
155	36.4	4.8	100925	9	AC012627	AC012627 Homo sapi
C 156	36.4	4.8	156583	9	AP006304	AP006304 Homo sapi
157	36.4	4.8	176099	9	AC108201	AC108201 Homo sapi
C 158	36.4	4.8	183031	10	AC126795	AC126795 Mus muscu
C 159	36.4	4.8	188215	2	AC025725	AC025725 Caenorhab
C 160	36.4	4.8	188616	3	AC084158	AC084158 Caenorhab
161	36.4	4.8	206136	9	AC068037	AC068037 Homo sapi
C 162	36.4	4.8	211750	9	AP006306	AP006306 Homo sapi
C 163	36.4	4.8	299081	2	AC006892	AC006892 Caenorhab
C 164	36.2	4.7	427	6	CQ455645	CQ455645 Sequence
165	36.2	4.7	494	9	HUMMSPO2	M34374 Homo sapien

166	36.2	4.7	1479	9	HSAL33356	AJ133356 Homo sapi
C 167	36.2	4.7	3274	6	BD193756	BD193756 Enterococ
168	36.2	4.7	3751	9	AF047368	AF047368 Homo sapi
169	36.2	4.7	70360	2	AC101122	AC101122 Mus muscu
170	36.2	4.7	110000	2	AC141459_2	Continuation (3 of
C 171	36.2	4.7	139469	2	AC143350	AC143350 Homo sapi
C 172	36.2	4.7	150222	2	BX942815	BX942815 Danio rer
173	36.2	4.7	150296	9	HUU91326	U91326 Homo sapien
C 174	36.2	4.7	153365	2	AC142443	AC142443 Homo sapi
C 175	36.2	4.7	154665	2	AC144355	AC144355 Homo sapi
C 176	36.2	4.7	158168	2	AC142544	AC142544 Homo sapi
177	36.2	4.7	161136	2	AC142078	AC142078 Homo sapi
C 178	36.2	4.7	172367	2	AC024457	AC024457 Homo sapi
179	36.2	4.7	177962	10	AC147251	AC147251 Mus muscu
180	36.2	4.7	180504	9	AL354793	AL354793 Human DNA
181	36.2	4.7	182402	2	AC116454	AC116454 Mus muscu
182	36.2	4.7	183285	10	AC128665	AC128665 Mus muscu
183	36.2	4.7	190015	9	AL450342	AL450342 Human DNA
C 184	36.2	4.7	195808	2	AC142442	AC142442 Homo sapi
185	36.2	4.7	196919	2	AC142542	AC142542 Homo sapi
186	36.2	4.7	206624	9	AP001825	AP001825 Homo sapi
187	36.2	4.7	220804	10	AC091283	AC091283 Mus muscu
188	36.2	4.7	243754	2	AC146822	AC146822 Ootlemur
189	36.2	4.7	326434	1	AE016947	AE016947 Enterococ
C 190	36	4.7	3145	10	BC054395	BC054395 Mus muscu
191	36	4.7	5807	6	AX346056	AX346056 Sequence
192	36	4.7	105087	9	AC093884	AC093884 Homo sapi
193	36	4.7	138603	2	AC034182	AC034182 Homo sapi
194	36	4.7	139215	8	AC126780	AC126780 Medicago
C 195	36	4.7	162556	9	AC006017	AC006017 Homo sapi
C 196	36	4.7	170346	2	CR555298	CR555298 Danio rer
C 197	36	4.7	174902	2	AC110071	AC110071 Homo sapi
198	36	4.7	182658	2	AC135844	AC135844 Felis cat
C 199	36	4.7	193708	9	AC005035	AC005035 Homo sapi
200	36	4.7	331039	3	AC116979	AC116979 Dictyoste
C 201	35.8	4.7	393	6	AR479582	AR479582 Sequence
202	35.8	4.7	832	6	AR415176	AR415176 Sequence
203	35.8	4.7	832	6	AX972010	AX972010 Sequence
204	35.8	4.7	832	6	BD110729	BD110729 EST and e
C 205	35.8	4.7	65114	9	AL590225	AL590225 Human DNA
C 206	35.8	4.7	86798	2	AL133317	AL133317 Mus muscu
C 207	35.8	4.7	102552	9	HS460G2	AL035446 Human DNA
C 208	35.8	4.7	110000	8	CR380951_2	Continuation (3 of
C 209	35.8	4.7	151792	10	AL365333	AL365333 Mouse DNA
C 210	35.8	4.7	162905	10	AC129318	AC129318 Mus muscu
C 211	35.8	4.7	173403	9	BS000114	BS000114 Pan trogl
C 212	35.8	4.7	175713	10	AL773587	AL773587 Mouse DNA
C 213	35.8	4.7	178193	2	AC068949	AC068949 Homo sapi
C 214	35.8	4.7	182426	2	BX571738	BX571738 Danio rer
C 215	35.8	4.7	186277	10	AC125154	AC125154 Mus muscu
216	35.8	4.7	193386	10	AC117693	AC117693 Mus muscu
217	35.8	4.7	248276	2	AC103007	AC103007 Rattus no
218	35.8	4.7	275820	2	AC112429	AC112429 Rattus no
C 219	35.6	4.6	400	11	G14360	G14360 SHGC-8871 H
220	35.6	4.6	10029	1	AE010608	AE010608 Fusobacte
C 221	35.6	4.6	29255	8	SPCC777	AL031532 S.pombe c
222	35.6	4.6	61475	2	AC100785	AC100785 Homo sapi
C 223	35.6	4.6	71661	10	AL954643	AL954643 Mouse DNA
224	35.6	4.6	110000	2	AC096496_2	Continuation (3 of
C 225	35.6	4.6	126746	9	AC008840	AC008840 Homo sapi
C 226	35.6	4.6	133120	9	HS393P23	Z95400 Human DNA s
227	35.6	4.6	160770	9	AC008511	AC008511 Homo sapi
C 228	35.6	4.6	162365	5	BX322622	BX322622 Zebrafish
C 229	35.6	4.6	167789	2	AC084260	AC084260 Homo sapi
230	35.6	4.6	167794	9	AC092472	AC092472 Homo sapi
231	35.6	4.6	170973	9	AC090097	AC090097 Homo sapi
C 232	35.6	4.6	182635	3	AC023729	AC023729 Drosophil
233	35.6	4.6	187230	3	AC023719	AC023719 Drosophil
C 234	35.6	4.6	219831	2	CR293498	CR293498 Danio rer
C 235	35.6	4.6	221189	2	AC131130	AC131130 Rattus no
C 236	35.6	4.6	236824	2	AC122632	AC122632 Rattus no
C 237	35.6	4.6	241687	2	AC096392	AC096392 Rattus no
C 238	35.6	4.6	255619	2	AC107503	AC107503 Rattus no

C 239	35.6	4.6	267991	2	AC112578	AC112578 Rattus no
C 240	35.6	4.6	270897	2	AC096415	AC096415 Rattus no
C 241	35.6	4.6	290970	3	AE003446	AE003446 Drosophil
C 242	35.4	4.6	1292	10	BC024451	BC024451 Mus muscu
C 243	35.4	4.6	1512	10	BC016446	BC016446 Mus muscu
C 244	35.4	4.6	2723	1	BGR439506	AJ439506 Bartonell
C 245	35.4	4.6	2725	1	BGR422079	AJ422079 Bartonell
C 246	35.4	4.6	27743	3	L10990	L10990 Caenorhabdi
C 247	35.4	4.6	103930	8	AY6323359	AY6323359 Gossypium
C 248	35.4	4.6	132505	2	AC015393	AC015393 Drosophil
C 249	35.4	4.6	151348	9	AC015807	AC015807 Homo sapi
C 250	35.4	4.6	153496	2	AC087044	AC087044 Homo sapi
C 251	35.4	4.6	153617	2	AC142619	AC142619 Macaca mu
C 252	35.4	4.6	162630	2	AC147730	AC147730 Oryctolag
C 253	35.4	4.6	163453	9	AC099561	AC099561 Homo sapi
C 254	35.4	4.6	172077	9	AC023514	AC023514 Homo sapi
C 255	35.4	4.6	172367	2	AC024457	AC024457 Homo sapi
C 256	35.4	4.6	172914	9	AP002791	AP002791 Homo sapi
C 257	35.4	4.6	173230	2	AC012216	AC012216 Homo sapi
C 258	35.4	4.6	175668	2	AC027268	AC027268 Homo sapi
C 259	35.4	4.6	179856	3	AC010067	AC010067 Drosophil
C 260	35.4	4.6	180222	9	AC009161	AC009161 Homo sapi
C 261	35.4	4.6	188379	9	AC026200	AC026200 Homo sapi
C 262	35.4	4.6	193372	9	AC026217	AC026217 Homo sapi
C 263	35.4	4.6	201531	9	AC026199	AC026199 Homo sapi
C 264	35.4	4.6	223754	5	BX323557	BX323557 Zebrafish
C 265	35.4	4.6	317354	3	AE003478	AE003478 Drosophil
C 266	35.2	4.6	10865	6	CQ807288	CQ807288 Sequence
C 267	35.2	4.6	84876	9	BX284698	BX284698 Human DNA
C 268	35.2	4.6	103347	9	AL136086	AL136086 Human DNA
C 269	35.2	4.6	110000	2	AC106945_2	Continuation (3 of
C 270	35.2	4.6	120787	8	AC002232	AC002232 Arabidops
C 271	35.2	4.6	132398	10	AC125278	AC125278 Mus muscu
C 272	35.2	4.6	136532	2	AC139597	AC139597 Rattus no
C 273	35.2	4.6	138062	9	AL161938	AL161938 Human DNA
C 274	35.2	4.6	139109	8	AP005051	AP005051 Oryza sat
C 275	35.2	4.6	158574	2	AC024895	AC024895 Homo sapi
C 276	35.2	4.6	161816	10	AL773547	AL773547 Mouse chr
C 277	35.2	4.6	164550	9	CNS01RHY	AL162633 Human chr
C 278	35.2	4.6	170427	2	AC006095	AC006095 Homo sapi
C 279	35.2	4.6	173067	9	AC026029	AC026029 Homo sapi
C 280	35.2	4.6	173921	9	AC084759	AC084759 Homo sapi
C 281	35.2	4.6	175274	9	AP004286	AP004286 Homo sapi
C 282	35.2	4.6	186183	9	AC026827	AC026827 Homo sapi
C 283	35.2	4.6	187061	2	AC122564	AC122564 Mus muscu
C 284	35.2	4.6	194718	9	AC011474	AC011474 Homo sapi
C 285	35.2	4.6	195234	2	AC141878	AC141878 Mus muscu
C 286	35.2	4.6	196085	2	AC025971	AC025971 Homo sapi
C 287	35.2	4.6	197650	2	AC027690	AC027690 Homo sapi
C 288	35.2	4.6	198278	2	AC010097	AC010097 Homo sapi
C 289	35.2	4.6	204524	2	AC055796	AC055796 Homo sapi
C 290	35.2	4.6	223182	5	AL929049	AL929049 Zebrafish
C 291	35.2	4.6	230701	2	AC096135	AC096135 Rattus no
C 292	35.2	4.6	247544	2	AC092741	AC092741 Mus muscu
C 293	35.2	4.6	253140	2	AC094055	AC094055 Rattus no
C 294	35.2	4.6	254575	2	AC127999	AC127999 Rattus no
C 295	35.2	4.6	269273	2	AC096095	AC096095 Rattus no
C 296	35.2	4.6	315079	1	MPULM03	AL445565 Mycoplasma
C 297	35.2	4.6	343882	2	AC114375	AC114375 Rattus no
C 298	35.2	4.6	509	11	BV012226	BV012226 MASC STS1
C 299	35	4.6	596	11	BV012227	BV012227 MASC STS1
C 300	35	4.6	794	5	AY522638	AY522638 Oreochrom
C 301	35	4.6	1627	8	AY102636	AY102636 Arabidops
C 302	35	4.6	2181	1	CACSPD	Z50009 C.acetobuty
C 303	35	4.6	2755	14	AY036009	AY036009 Hollyhock
C 304	35	4.6	42434	3	AF045641	AF045641 Caenorhab
C 305	35	4.6	68790	9	HSJ287H17	AL121970 Human DNA
C 306	35	4.6	86436	8	AC007323	AC007323 Genomic s
C 307	35	4.6	104364	8	AC006919	AC006919 Arabidops
C 308	35	4.6	117189	2	AC147547	AC147547 Rattus no
C 309	35	4.6	156134	2	BX927097	BX927097 Danio rer
C 310	35	4.6	169207	10	AC119813	AC119813 Mus muscu
C 311	35					

C 312	35	4.6	171518	2	AL589697	AL589697 Homo sapi
C 313	35	4.6	174347	10	AL928956	AL928956 Mouse DNA
C 314	35	4.6	176508	9	AL365498	AL365498 Human DNA
C 315	35	4.6	177004	2	AC129114	AC129114 Rattus no
C 316	35	4.6	179085	9	AC011611	AC011611 Homo sapi
C 317	35	4.6	183137	9	AC008734	AC008734 Homo sapi
C 318	35	4.6	184809	9	BS000097	BS000097 Pan trogl
C 319	35	4.6	185276	2	AC136050	AC136050 Rattus no
C 320	35	4.6	188858	9	AC090621	AC090621 Homo sapi
C 321	35	4.6	189867	2	AC128902	AC128902 Rattus no
C 322	35	4.6	192390	2	AC102900	AC102900 Mus muscu
C 323	35	4.6	197431	9	AL360157	AL360157 Human DNA
C 324	35	4.6	201948	2	AC142435	AC142435 Rattus no
C 325	35	4.6	202392	2	AC021018	AC021018 Homo sapi
C 326	35	4.6	208281	2	AC106260	AC106260 Rattus no
C 327	35	4.6	211621	2	AC127128	AC127128 Rattus no
C 328	35	4.6	219228	2	AC123889	AC123889 Rattus no
C 329	35	4.6	220737	2	AC128459	AC128459 Rattus no
C 330	35	4.6	242885	2	AC097836	AC097836 Rattus no
C 331	35	4.6	250029	3	AE014820	AE014820 Plasmodiu
C 332	35	4.6	258263	2	AC097043	AC097043 Rattus no
C 333	35	4.6	259902	2	AC102170	AC102170 Mus muscu
C 334	35	4.6	259967	2	AC105625	AC105625 Rattus no
C 335	35	4.6	265061	2	AC123375	AC123375 Rattus no
C 336	35	4.6	266766	2	AC094770	AC094770 Rattus no
C 337	35	4.6	281307	2	AC106352	AC106352 Rattus no
C 338	35	4.6	299015	2	AC006842	AC006842 Caenorhab
C 339	34.8	4.5	852	6	AX954037	AX954037 Sequence
C 340	34.8	4.5	870	6	AX953487	AX953487 Sequence
C 341	34.8	4.5	1809	6	AR452918	AR452918 Sequence
C 342	34.8	4.5	1809	6	AX060647	AX060647 Sequence
C 343	34.8	4.5	1809	8	AF364866	AF364866 Helianthu
C 344	34.8	4.5	5055	10	AF162282	AF162282 Mus muscu
C 345	34.8	4.5	5249	10	BC053047	BC053047 Mus muscu
C 346	34.8	4.5	5254	10	AF036007	AF036007 Mus muscu
C 347	34.8	4.5	5261	10	BC048148	BC048148 Mus muscu
C 348	34.8	4.5	5267	10	MMDNAMET	X14805 Mus musculu
C 349	34.8	4.5	5543	10	AF175432	AF175432 Mus muscu
C 350	34.8	4.5	5877	10	AF036009	AF036009 Mus muscu
C 351	34.8	4.5	11130	1	AE009996	AE009996 Streptoco
C 352	34.8	4.5	11131	1	AE006511	AE006511 Streptoco
C 353	34.8	4.5	31434	3	CEY68A4A	AL021503 Caenorhab
C 354	34.8	4.5	34971	2	AC149340	AC149340 Phakopsor
C 355	34.8	4.5	50029	1	AE014144	AE014144 Streptoco
C 356	34.8	4.5	50466	2	AC136370	AC136370 Homo sapi
C 357	34.8	4.5	50466	2	AC136370	AC136370 Homo sapi
C 358	34.8	4.5	57180	8	ATF18D22	AL360334 Arabidops
C 359	34.8	4.5	63939	9	AL359200	AL359200 Human DNA
C 360	34.8	4.5	70805	8	AP006129	AP006129 Lotus cor
C 361	34.8	4.5	77567	8	ATT19F6	AL109619 Arabidops
C 362	34.8	4.5	90246	2	AC022686	AC022686 Homo sapi
C 363	34.8	4.5	94125	9	AC016966	AC016966 Homo sapi
C 364	34.8	4.5	97711	8	ATT16K5	AL132965 Arabidops
C 365	34.8	4.5	98505	8	AP006692	AP006692 Lotus cor
C 366	34.8	4.5	109043	5	CNS08CA7	AL808032 BAC 30B15
C 367	34.8	4.5	109398	9	AC044817	AC044817 Homo sapi
C 368	34.8	4.5	110000	1	CP000003_04	Continuation (5 of
C 369	34.8	4.5	116156	8	ATAC002343	AC002343 Arabidops
C 370	34.8	4.5	127501	2	AL357852	AL357852 Homo sapi
C 371	34.8	4.5	131286	4	AB053451	AB053451 Sus scrof
C 372	34.8	4.5	139378	9	HS64K7	AL031668 Human DNA
C 373	34.8	4.5	143687	9	AC106793	AC106793 Homo sapi
C 374	34.8	4.5	154137	2	AC139735	AC139735 Canis fam
C 375	34.8	4.5	154936	2	AC137907	AC137907 Canis fam
C 376	34.8	4.5	156630	9	BS000087	BS000087 Pan trogl
C 377	34.8	4.5	160676	2	AC022920	AC022920 Homo sapi
C 378	34.8	4.5	162087	2	AC011576	AC011576 Homo sapi
C 379	34.8	4.5	165333	2	CR626869	CR626869 Danio rer
C 380	34.8	4.5	168311	2	AC087788	AC087788 Homo sapi
C 381	34.8	4.5	168366	2	AC069409	AC069409 Homo sapi
C 382	34.8	4.5	168843	9	AC068207	AC068207 Homo sapi
C 383	34.8	4.5	169637	9	AC113412	AC113412 Homo sapi
C 384	34.8	4.5	169964	9	AC055710	AC055710 Homo sapi

C 385	34.8	4.5	171545	9	AC008394	AC008394 Homo sapi
386	34.8	4.5	171899	2	AC020562	AC020562 Homo sapi
C 387	34.8	4.5	172650	2	AC040920	AC040920 Homo sapi
388	34.8	4.5	174926	9	AC093847	AC093847 Homo sapi
389	34.8	4.5	176512	9	AC012323	AC012323 Homo sapi
390	34.8	4.5	177681	5	BX005052	BX005052 Zebrafish
391	34.8	4.5	177770	9	AC110027	AC110027 Homo sapi
392	34.8	4.5	177872	10	AC093371	AC093371 Genomic s
393	34.8	4.5	180606	2	AC073406	AC073406 Homo sapi
394	34.8	4.5	180684	9	AC135626	AC135626 Homo sapi
C 395	34.8	4.5	191988	2	AC135980	AC135980 Homo sapi
396	34.8	4.5	196677	8	ATCHRIV60	AL161560 Arabidops
397	34.8	4.5	197864	9	HSY214H10	AL022344 Human DNA
C 398	34.8	4.5	205642	2	AC007898	AC007898 Homo sapi
C 399	34.8	4.5	205831	2	AC074192	AC074192 Homo sapi
400	34.8	4.5	206852	9	AC091182	AC091182 Homo sapi
401	34.8	4.5	211005	2	AC118299	AC118299 Rattus no
402	34.8	4.5	214303	2	AC124993	AC124993 Mus muscu
403	34.8	4.5	226067	2	AC138358	AC138358 Mus muscu
C 404	34.8	4.5	241629	2	AC107491	AC107491 Rattus no
C 405	34.8	4.5	243065	2	AC112818	AC112818 Rattus no
406	34.8	4.5	243072	6	AX770904	AX770904 Sequence
407	34.8	4.5	249995	3	AE014840	AE014840 Plasmodiu
408	34.8	4.5	252161	2	AC129382	AC129382 Rattus no
409	34.8	4.5	262852	2	AC096331	AC096331 Rattus no
410	34.8	4.5	282915	2	AC098165	AC098165 Rattus no
411	34.8	4.5	325650	1	AP005145	AP005145 Streptoco
C 412	34.8	4.5	349318	1	BX571863	BX571863 Phototrab
413	34.6	4.5	6981	5	DYGCALB	L12532 Discopyge o
414	34.6	4.5	16545	6	AX344953	AX344953 Sequence
C 415	34.6	4.5	46778	9	AL356003	AL356003 Human DNA
C 416	34.6	4.5	98078	9	AL451083	AL451083 Human DNA
417	34.6	4.5	99592	9	AF263284	AF263284 Homo sapi
C 418	34.6	4.5	104630	9	AC007848	AC007848 Homo sapi
C 419	34.6	4.5	106434	8	AP004847	AP004847 Oryza sat
C 420	34.6	4.5	122404	2	AC136155	AC136155 Rattus no
C 421	34.6	4.5	128861	5	BX294435	BX294435 Zebrafish
422	34.6	4.5	150295	5	BX005103	BX005103 Zebrafish
C 423	34.6	4.5	154256	5	BX511192	BX511192 Zebrafish
424	34.6	4.5	155378	2	AC023536	AC023536 Homo sapi
425	34.6	4.5	156150	2	CR524827	CR524827 Danio rer
426	34.6	4.5	158255	2	AC025695	AC025695 Homo sapi
C 427	34.6	4.5	160295	10	AC122884	AC122884 Mus muscu
428	34.6	4.5	162472	9	CNS01DUW	AL133371 Human chr
C 429	34.6	4.5	166000	9	AL390731	AL390731 Human DNA
C 430	34.6	4.5	168247	9	AC005014	AC005014 Homo sapi
C 431	34.6	4.5	168571	9	CNS01DUF	AL133249 BAC seque
C 432	34.6	4.5	169010	10	AL672260	AL672260 Mouse DNA
C 433	34.6	4.5	169720	2	AC024458	AC024458 Homo sapi
434	34.6	4.5	171490	2	AC022481	AC022481 Homo sapi
C 435	34.6	4.5	171747	10	AC132412	AC132412 Mus muscu
436	34.6	4.5	174801	9	AL445238	AL445238 Human DNA
C 437	34.6	4.5	175151	9	AL160152	AL160152 Human DNA
438	34.6	4.5	176155	2	AC020879	AC020879 Mus muscu
439	34.6	4.5	176724	2	AL359772	AL359772 Homo sapi
C 440	34.6	4.5	179068	10	AL627125	AL627125 Mouse DNA
441	34.6	4.5	181850	9	AC018680	AC018680 Homo sapi
C 442	34.6	4.5	182703	2	AC073117	AC073117 Homo sapi
443	34.6	4.5	187204	9	AC084082	AC084082 Homo sapi
444	34.6	4.5	190585	2	AC109303	AC109303 Mus muscu
445	34.6	4.5	192800	2	AC113288	AC113288 Mus muscu
C 446	34.6	4.5	233118	2	AC140327	AC140327 Mus muscu
447	34.6	4.5	235412	2	AC106607	AC106607 Rattus no
448	34.6	4.5	237831	2	AC113715	AC113715 Rattus no
C 449	34.6	4.5	242118	2	AC106908	AC106908 Rattus no
450	34.6	4.5	245424	2	AC112822	AC112822 Rattus no
C 451	34.6	4.5	278946	2	AC115321	AC115321 Rattus no
452	34.6	4.5	295639	2	AL360019	AL360019 Homo sapi
453	34.6	4.5	325076	2	AC125912	AC125912 Rattus no
C 454	34.6	4.5	346970	2	BX510643	BX510643 Danio rer
C 455	34.4	4.5	734	14	AY556458	AY556458 Thielavio
C 456	34.4	4.5	1413	6	AX489469	AX489469 Sequence
457	34.4	4.5	1798	5	BC073257	BC073257 Xenopus l

C 458	34.4	4.5	2711	10	BC005616	BC005616 Mus muscu
459	34.4	4.5	32428	10	AF285839S1	AF285839 Mus muscu
460	34.4	4.5	60554	2	AC101366	AC101366 Mus muscu
461	34.4	4.5	74269	2	AC136368	AC136368 Homo sapi
462	34.4	4.5	84122	9	AL133463	AL133463 Human DNA
C 463	34.4	4.5	85693	2	AC124117	AC124117 Mus muscu
C 464	34.4	4.5	88619	9	AC097723	AC097723 Homo sapi
465	34.4	4.5	96726	2	HS1178F13	AL118500 Homo sapi
466	34.4	4.5	102842	10	AL671903	AL671903 Mouse DNA
467	34.4	4.5	125020	9	AF429315	AF429315 Homo sapi
C 468	34.4	4.5	128000	2	AC004046	AC004046 Homo sapi
C 469	34.4	4.5	139131	2	AP004385	AP004385 Oryza sat
470	34.4	4.5	143756	9	AC136365	AC136365 Homo sapi
C 471	34.4	4.5	149577	9	AP005902	AP005902 Homo sapi
C 472	34.4	4.5	150399	9	AC093680	AC093680 Homo sapi
473	34.4	4.5	152324	2	AC136938	AC136938 Homo sapi
474	34.4	4.5	154675	2	CR354440	CR354440 Danio rer
475	34.4	4.5	156612	2	AC147212	AC147212 Pan trogl
476	34.4	4.5	156902	2	AC073630	AC073630 Homo sapi
C 477	34.4	4.5	164363	2	AC073229	AC073229 Homo sapi
C 478	34.4	4.5	164688	2	AC138727	AC138727 Pongo pyg
479	34.4	4.5	168117	10	AC132352	AC132352 Mus muscu
480	34.4	4.5	168278	10	AC126246	AC126246 Mus muscu
C 481	34.4	4.5	169453	9	AC096558	AC096558 Homo sapi
C 482	34.4	4.5	172265	2	CR376845	CR376845 Danio rer
483	34.4	4.5	172695	9	AC068303	AC068303 Homo sapi
484	34.4	4.5	173357	9	AC113145	AC113145 Homo sapi
C 485	34.4	4.5	175952	9	AC069285	AC069285 Homo sapi
C 486	34.4	4.5	176293	8	AP005158	AP005158 Oryza sat
C 487	34.4	4.5	177537	2	CR407599	CR407599 Danio rer
C 488	34.4	4.5	178752	9	AC021889	AC021889 Homo sapi
489	34.4	4.5	180424	9	AC106860	AC106860 Homo sapi
C 490	34.4	4.5	180588	5	AL954672	AL954672 Zebrafish
491	34.4	4.5	182178	9	AL138711	AL138711 Human DNA
492	34.4	4.5	185161	2	AC116732	AC116732 Mus muscu
C 493	34.4	4.5	191265	2	AC068996	AC068996 Homo sapi
494	34.4	4.5	191373	9	AC017067	AC017067 Homo sapi
C 495	34.4	4.5	192638	2	AC101861	AC101861 Mus muscu
C 496	34.4	4.5	194437	2	AC117948	AC117948 Homo sapi
497	34.4	4.5	195408	2	AC109270	AC109270 Mus muscu
C 498	34.4	4.5	196356	10	AC102637	AC102637 Mus muscu
499	34.4	4.5	196566	10	AL663045	AL663045 Mouse DNA
500	34.4	4.5	197775	9	AC012366	AC012366 Homo sapi
501	34.4	4.5	201307	2	AC141181	AC141181 Rattus no
C 502	34.4	4.5	203626	2	AC138730	AC138730 Pongo pyg
503	34.4	4.5	203715	2	AC018807	AC018807 Homo sapi
504	34.4	4.5	213387	2	AC109275	AC109275 Mus muscu
505	34.4	4.5	213857	2	AC126310	AC126310 Rattus no
C 506	34.4	4.5	215553	2	AC092716	AC092716 Mus muscu
C 507	34.4	4.5	229829	2	AC055749	AC055749 Homo sapi
508	34.4	4.5	231239	2	AC133164	AC133164 Mus muscu
C 509	34.4	4.5	235867	2	AC140226	AC140226 Mus muscu
C 510	34.4	4.5	244678	2	AC127664	AC127664 Rattus no
C 511	34.4	4.5	248015	2	AC127748	AC127748 Rattus no
512	34.4	4.5	248164	2	AC096228	AC096228 Rattus no
C 513	34.4	4.5	250029	3	AE014838	AE014838 Plasmodiu
514	34.4	4.5	251086	2	AC099142	AC099142 Rattus no
C 515	34.4	4.5	253932	2	AC120488	AC120488 Rattus no
C 516	34.2	4.5	1393	1	AF522261	AF522261 Haemophil
C 517	34.2	4.5	1477	1	AF522260	AF522260 Haemophil
C 518	34.2	4.5	1477	1	HIIGAA66	X82467 H.influenza
519	34.2	4.5	2153	5	AF287486	AF287486 Oncorhync
520	34.2	4.5	2155	5	AF115521	AF115521 Oncorhync
C 521	34.2	4.5	2607	3	AY345039	AY345039 Aldisa ba
522	34.2	4.5	16710	8	AY459338	AY459338 Oryza sat
523	34.2	4.5	26498	1	AE000792	AE000792 Borrelia
524	34.2	4.5	27999	8	SPCC70	AL023794 S.pombe c
C 525	34.2	4.5	58789	2	AC131580	AC131580 Mus muscu
C 526	34.2	4.5	64512	9	AP000255	AP000255 Homo sapi
527	34.2	4.5	64672	2	AC100019	AC100019 Mus muscu
528	34.2	4.5	76089	2	AC124285	AC124285 Homo sapi
C 529	34.2	4.5	83848	10	AF246978	AF246978 Mus muscu
C 530	34.2	4.5	85268	2	AC022648	AC022648 Homo sapi

531	34.2	4.5	90551	10	AL928543	AL928543 Mouse DNA
C 532	34.2	4.5	100000	9	AP000213	AP000213 Homo sapi
C 533	34.2	4.5	110000	2	Continuation (3 of	Continuation (3 of
C 534	34.2	4.5	110000	6	Continuation (5 of	Continuation (5 of
535	34.2	4.5	117542	2	AC023193	AC023193 Mus muscu
536	34.2	4.5	120016	8	AP004929	AP004929 Lotus cor
C 537	34.2	4.5	126470	9	AL390234	AL390234 Human DNA
C 538	34.2	4.5	132585	9	AC131947	AC131947 Homo sapi
539	34.2	4.5	136653	9	AC026776	AC026776 Homo sapi
540	34.2	4.5	136653	9	AC090111	AC090111 Homo sapi
C 541	34.2	4.5	138338	9	AC146073	AC146073 Pan trogl
C 542	34.2	4.5	147420	2	AC116850	AC116850 Mus muscu
543	34.2	4.5	147715	9	AC022534	AC022534 Homo sapi
C 544	34.2	4.5	147733	2	AC101914	AC101914 Mus muscu
C 545	34.2	4.5	149298	9	AP000031	AP000031 Homo sapi
C 546	34.2	4.5	160004	9	AL139318	AL139318 Human DNA
C 547	34.2	4.5	162150	9	AC093877	AC093877 Homo sapi
548	34.2	4.5	163566	4	AC139340	AC139340 Ateles
549	34.2	4.5	167364	10	AC121590	AC121590 Mus muscu
550	34.2	4.5	168725	2	AC134536	AC134536 Mus muscu
551	34.2	4.5	173492	2	AC111329	AC111329 Rattus no
552	34.2	4.5	174092	2	AC069129	AC069129 Homo sapi
553	34.2	4.5	174311	9	AC016816	AC016816 Homo sapi
C 554	34.2	4.5	175467	2	AC079215	AC079215 Homo sapi
C 555	34.2	4.5	176051	9	AC022008	AC022008 Homo sapi
556	34.2	4.5	177034	8	CNS08CAC	AL831799 Oryza sat
C 557	34.2	4.5	179200	2	AC134838	AC134838 Mus muscu
558	34.2	4.5	180404	2	AC102167	AC102167 Mus muscu
C 559	34.2	4.5	181557	10	AC069014	AC069014 Mus muscu
560	34.2	4.5	181683	10	AC122180	AC122180 Mus muscu
561	34.2	4.5	182228	10	AC036145	AC036145 Mus muscu
562	34.2	4.5	183101	9	AC021915	AC021915 Homo sapi
563	34.2	4.5	184738	9	AL162574	AL162574 Human DNA
564	34.2	4.5	184794	5	AL929229	AL929229 Zebrafish
C 565	34.2	4.5	185277	10	AC098567	AC098567 Genomic S
C 566	34.2	4.5	186014	5	BX908749	BX908749 Zebrafish
C 567	34.2	4.5	186296	2	AC117907	AC117907 Rattus no
C 568	34.2	4.5	186719	2	CR628370	CR628370 Danio rer
569	34.2	4.5	188891	2	AC021156	AC021156 Homo sapi
570	34.2	4.5	190379	2	AC022386	AC022386 Homo sapi
C 571	34.2	4.5	190630	9	AC117470	AC117470 Homo sapi
572	34.2	4.5	190927	2	AC141748	AC141748 Apis mell
573	34.2	4.5	193188	9	AC092140	AC092140 Homo sapi
574	34.2	4.5	193892	2	AC073037	AC073037 Homo sapi
C 575	34.2	4.5	194815	9	AL136295	AL136295 Human chr
C 576	34.2	4.5	195211	2	CR352256	CR352256 Danio rer
577	34.2	4.5	195425	10	AC125399	AC125399 Mus muscu
578	34.2	4.5	195667	10	AC073918	AC073918 Mus muscu
579	34.2	4.5	200222	2	AC023555	AC023555 Homo sapi
580	34.2	4.5	206075	2	AC120361	AC120361 Mus muscu
C 581	34.2	4.5	207960	10	AC124173	AC124173 Mus muscu
C 582	34.2	4.5	211668	2	AC115146	AC115146 Rattus no
C 583	34.2	4.5	216217	10	AC107231	AC107231 Mus muscu
C 584	34.2	4.5	218866	2	BX323890	BX323890 Mus muscu
585	34.2	4.5	225514	2	AC024142	AC024142 Mus muscu
C 586	34.2	4.5	226711	2	AC127440	AC127440 Rattus no
587	34.2	4.5	227753	2	AC102131	AC102131 Mus muscu
C 588	34.2	4.5	231382	2	AC095549	AC095549 Rattus no
C 589	34.2	4.5	233358	2	AC095317	AC095317 Rattus no
590	34.2	4.5	239847	10	AL591466	AL591466 Mouse DNA
C 591	34.2	4.5	246688	2	AC112282	AC112282 Rattus no
C 592	34.2	4.5	253751	2	AC051621	AC051621 Mus muscu
593	34.2	4.5	256381	2	AC013610	AC013610 Homo sapi
594	34.2	4.5	278521	2	AC092715	AC092715 Homo sapi
C 595	34.2	4.5	340000	9	AP001712	AP001712 Homo sapi
C 596	34.2	4.5	349980	6	AX696302	AX696302 Sequence
597	34	4.4	1283	3	AF132555	AF132555 Drosophil
598	34	4.4	1599	8	AK065805	AK065805 Oryza sat
599	34	4.4	2918	8	AK103210	AK103210 Oryza sat
C 600	34	4.4	4843	2	AC014531	AC014531 Drosophil
C 601	34	4.4	5791	10	MMU65403	U65403 Mus musculu
C 602	34	4.4	24142	6	AX537050	AX537050 Sequence
603	34	4.4	43801	3	U28740	U28740 Caenorhabdi

C 604	34	4.4	59818	4	AC123967	AC123967 Smnthops
605	34	4.4	60962	2	AC103742	AC103742 Homo sapi
606	34	4.4	79459	3	AC089995	AC089995 Caenorhab
C 607	34	4.4	103196	3	AC023738	AC023738 Drosophil
C 608	34	4.4	110000	8	CR382136_03	Continuation (4 of
609	34	4.4	110000	8	CR382137_00	CR382137 Debaryomy
610	34	4.4	110000	8	AY506529_0	AY506529 Zea mays
C 611	34	4.4	120583	8	OSJN00125	AL606998 Oryza sat
612	34	4.4	134482	2	AC109786	AC109786 Bos tauru
613	34	4.4	141009	2	AC109915	AC109915 Bos tauru
C 614	34	4.4	142607	2	AC113578	AC113578 Tetraodon
C 615	34	4.4	143153	2	AC025027	AC025027 Homo sapi
616	34	4.4	144807	2	AC147413	AC147413 Homo sapi
C 617	34	4.4	145766	8	OSJN00287	AL731644 Oryza sat
C 618	34	4.4	149904	9	CNS01DSV	AL122020 Human chr
C 619	34	4.4	150864	8	OSJN00053	AL606623 Oryza sat
620	34	4.4	150892	5	AL929190	AL929190 Zebrafish
621	34	4.4	152217	5	BX005104	BX005104 Zebrafish
622	34	4.4	152776	2	BX897743	BX897743 Danio rer
623	34	4.4	152829	9	AC078793	AC078793 Homo sapi
C 624	34	4.4	153607	2	AL355523	AL355523 Homo sapi
C 625	34	4.4	154348	4	AC129961	AC129961 Sus scrof
626	34	4.4	157176	9	AC007092	AC007092 Homo sapi
C 627	34	4.4	158498	8	OSJN00300	BX842603 Oryza sat
C 628	34	4.4	158504	2	AC107810	AC107810 Mus muscu
629	34	4.4	158861	10	AL845273	AL845273 Mouse DNA
630	34	4.4	159422	2	CR391981	CR391981 Danio rer
C 631	34	4.4	160461	2	AC125270	AC125270 Mus muscu
C 632	34	4.4	161514	10	BX004793	BX004793 Mouse DNA
633	34	4.4	162633	2	AC148483	AC148483 Medicago
634	34	4.4	166989	8	AP005836	AP005836 Oryza sat
C 635	34	4.4	167148	5	BX088714	BX088714 Zebrafish
636	34	4.4	167663	9	AC093854	AC093854 Homo sapi
637	34	4.4	167778	2	AC132618	AC132618 Mus muscu
638	34	4.4	173413	2	AC145309	AC145309 Homo sapi
C 639	34	4.4	177248	5	AL929093	AL929093 Zebrafish
640	34	4.4	182025	9	AL138900	AL138900 Human DNA
641	34	4.4	182144	9	AC009223	AC009223 Homo sapi
C 642	34	4.4	182820	10	AC122446	AC122446 Mus muscu
C 643	34	4.4	183092	5	AC145912	AC145912 Gallus ga
C 644	34	4.4	187144	2	BX957353	BX957353 Danio rer
645	34	4.4	187674	2	AC013748	AC013748 Homo sapi
646	34	4.4	189538	10	AC116787	AC116787 Mus muscu
647	34	4.4	193091	8	AP005508	AP005508 Oryza sat
648	34	4.4	195068	10	AC019153	AC019153 Mus muscu
649	34	4.4	196053	10	AC117684	AC117684 Mus muscu
C 650	34	4.4	197109	10	AC122239	AC122239 Mus muscu
651	34	4.4	197611	9	AL390840	AL390840 Human DNA
652	34	4.4	197859	2	AC137159	AC137159 Rattus no
C 653	34	4.4	198445	2	BX927295	BX927295 Danio rer
C 654	34	4.4	198523	10	AL845158	AL845158 Mouse DNA
655	34	4.4	199844	5	AL929319	AL929319 Zebrafish
C 656	34	4.4	199912	2	AC141558	AC141558 Mus muscu
657	34	4.4	200000	9	AB019440	AB019440 Homo sapi
C 658	34	4.4	201299	9	AC007158	AC007158 Homo sapi
C 659	34	4.4	203257	5	BX000993	BX000993 Zebrafish
C 660	34	4.4	206524	2	AC141649	AC141649 Rattus no
C 661	34	4.4	209058	2	AC109267	AC109267 Mus muscu
C 662	34	4.4	212485	10	AC090122	AC090122 Mus muscu
663	34	4.4	215399	2	AC116268	AC116268 Rattus no
C 664	34	4.4	220430	2	AC095315	AC095315 Rattus no
C 665	34	4.4	226762	2	AC128126	AC128126 Rattus no
666	34	4.4	227353	2	AC141259	AC141259 Homo sapi
C 667	34	4.4	230392	9	AC026672	AC026672 Homo sapi
668	34	4.4	231589	2	AC118944	AC118944 Rattus no
C-669	34	4.4	234053	2	AC128262	AC128262 Rattus no
C 670	34	4.4	236013	2	AC106499	AC106499 Rattus no
C 671	34	4.4	240079	2	AC128364	AC128364 Rattus no
672	34	4.4	243782	2	BX548019	BX548019 Danio rer
673	34	4.4	246893	2	AC132513	AC132513 Rattus no
674	34	4.4	252480	2	AC103661	AC103661 Mus muscu
C 675	34	4.4	256703	2	AC114076	AC114076 Rattus no
C 676	34	4.4	257816	2	AC131814	AC131814 Rattus no

C 677	34	4.4	259464	2	AC107525	AC107525 Rattus no	750	33.8	4.4	193057	9	AC022441	AC022441 Homo sapi
678	34	4.4	259599	2	AC123087	AC123087 Rattus no	751	33.8	4.4	193963	9	AC007336	AC007336 Homo sapi
679	34	4.4	262101	2	AC113760	AC113760 Rattus no	752	33.8	4.4	195635	9	AC017101	AC017101 Homo sapi
680	34	4.4	263877	2	AC128535	AC128535 Rattus no	753	33.8	4.4	196392	2	AC120322	AC120322 Rattus no
C 681	34	4.4	264412	2	AC128074	AC128074 Rattus no	754	33.8	4.4	196554	2	AC137110	AC137110 Mus muscu
682	34	4.4	288721	3	AE003447	AE003447 Drosophil	C 755	33.8	4.4	197895	2	AC117894	AC117894 Rattus no
C 683	34	4.4	294339	2	AC105885	AC105885 Rattus no	756	33.8	4.4	199104	5	AL929266	AL929266 Zebrafish
C 684	34	4.4	312946	2	AC109691	AC109691 Rattus no	757	33.8	4.4	203393	2	AC101691	AC101691 Mus muscu
C 685	34	4.4	319828	2	AC096270	AC096270 Rattus no	758	33.8	4.4	205306	10	AC131737	AC131737 Mus muscu
C 686	34	4.4	330350	3	PFA929353	AL929353 Plasmodiu	759	33.8	4.4	205640	10	AC133205	AC133205 Mus muscu
C 687	34	4.4	346077	2	AC106235	AC106235 Rattus no	760	33.8	4.4	209643	10	AC079438	AC079438 Mus muscu
C 688	34	4.4	346354	2	AC095850	AC095850 Rattus no	761	33.8	4.4	213721	9	HS172B20	AL022319 Human DNA
689	33.8	4.4	575	6	CQ072807	CQ072807 Sequence	C 762	33.8	4.4	215390	10	AL672089	AL672089 Mouse DNA
690	33.8	4.4	575	6	CQ103614	CQ103614 Sequence	C 763	33.8	4.4	220464	2	AC115409	AC115409 Rattus no
691	33.8	4.4	575	6	CQ142446	CQ142446 Sequence	764	33.8	4.4	220994	2	AC128964	AC128964 Rattus no
692	33.8	4.4	575	6	CQ225686	CQ225686 Sequence	765	33.8	4.4	221489	2	AC107577	AC107577 Rattus no
693	33.8	4.4	575	6	CQ263717	CQ263717 Sequence	766	33.8	4.4	222972	2	BX511082	BX511082 Danio rer
694	33.8	4.4	575	6	CQ300796	CQ300796 Sequence	767	33.8	4.4	225983	2	AC113937	AC113937 Mus muscu
695	33.8	4.4	575	6	CQ338087	CQ338087 Sequence	C 768	33.8	4.4	227441	2	CR589875	CR589875 Danio rer
C 696	33.8	4.4	1103	9	AF066051	AF066051 Homo sapi	769	33.8	4.4	227631	10	AC115692	AC115692 Mus muscu
C 697	33.8	4.4	1265	8	HVU277097	AJ277097 Hordeum v	770	33.8	4.4	227853	2	AC114204	AC114204 Rattus no
698	33.8	4.4	43708	9	AC118345	AC118345 Homo sapi	771	33.8	4.4	230365	2	AC121415	AC121415 Rattus no
C 699	33.8	4.4	52947	2	AC068354	AC068354 Homo sapi	772	33.8	4.4	233994	2	AC111450	AC111450 Rattus no
700	33.8	4.4	59413	2	AC136535	AC136535 Rattus no	C 773	33.8	4.4	236846	2	AC095590	AC095590 Rattus no
701	33.8	4.4	60016	2	AC126381	AC126381 Homo sapi	774	33.8	4.4	240673	2	AC132745	AC132745 Rattus no
C 702	33.8	4.4	65674	5	BX936427	BX936427 Zebrafish	775	33.8	4.4	240970	2	AC111859	AC111859 Rattus no
C 703	33.8	4.4	73228	9	AL391807	AL391807 Human DNA	C 776	33.8	4.4	243249	2	AC097383	AC097383 Rattus no
C 704	33.8	4.4	77439	9	HS127F18	AL031575 Human DNA	C 777	33.8	4.4	243409	2	AC098607	AC098607 Rattus no
C 705	33.8	4.4	78456	10	AL627393	AL627393 Mouse DNA	C 778	33.8	4.4	243573	2	AC134068	AC134068 Rattus no
706	33.8	4.4	79943	9	AL353664	AL353664 Human DNA	C 779	33.8	4.4	245636	2	AC095871	AC095871 Rattus no
707	33.8	4.4	85144	9	AC125621	AC125621 Homo sapi	C 780	33.8	4.4	250537	2	AC099097	AC099097 Rattus no
C 708	33.8	4.4	85166	2	AC008617	AC008617 Homo sapi	C 781	33.8	4.4	255281	2	AC111799	AC111799 Rattus no
709	33.8	4.4	103476	2	AC027350	AC027350 Homo sapi	C 782	33.8	4.4	259685	2	AC063928	AC063928 Homo sapi
C 710	33.8	4.4	103505	2	AC026788	AC026788 Homo sapi	C 783	33.8	4.4	263038	2	AC110337	AC110337 Rattus no
711	33.8	4.4	105608	2	AC116396	AC116396 Mus muscu	C 784	33.8	4.4	277481	2	AC118399	AC118399 Rattus no
C 712	33.8	4.4	110000	2	AC095857_3	Continuation (4 of	C 785	33.8	4.4	281806	2	AC095151	AC095151 Rattus no
713	33.8	4.4	110000	2	AC105793_0	AC105793 Rattus no	786	33.8	4.4	288968	2	AC115432	AC115432 Rattus no
714	33.8	4.4	110804	9	AC004748	AC004748 Homo sapi	787	33.8	4.4	290670	2	AC121043	AC121043 Rattus no
C 715	33.8	4.4	125859	9	AL354695	AL354695 Human DNA	788	33.8	4.4	334935	2	AC134352	AC134352 Rattus no
716	33.8	4.4	127411	2	AC129780	AC129780 Mus muscu	C 789	33.8	4.4	347050	3	PFA929351	AL929351 Plasmodiu
C 717	33.8	4.4	137173	2	AC016631	AC016631 Homo sapi	790	33.6	4.4	373	6	CQ681831	CQ681831 Sequence
718	33.8	4.4	142903	2	AL627254	AL627254 Danio rer	C 791	33.6	4.4	1010	9	HSKRT4GEN	X97566 Homo sapien
719	33.8	4.4	144722	9	AC008831	AC008831 Homo sapi	792	33.6	4.4	3316	10	BC061692	BC061692 Mus muscu
C 720	33.8	4.4	153176	9	AC118465	AC118465 Homo sapi	C 793	33.6	4.4	3666	1	AF319618	AF319618 Vibrio fi
721	33.8	4.4	157039	9	AL138893	AL138893 Human DNA	794	33.6	4.4	5194	5	XELRAG1X	L19324 Xenopus lae
722	33.8	4.4	158305	9	CNS07EFA	AL512361 Human chr	795	33.6	4.4	6244	1	AE010136	AE010136 Pyrococcu
723	33.8	4.4	159713	2	AC120920	AC120920 Rattus no	C 796	33.6	4.4	10029	1	AE006364	AE006364 Lactococc
C 724	33.8	4.4	161370	9	AC093800	AC093800 Homo sapi	C 797	33.6	4.4	10805	1	AE013048	AE013048 Thermoana
725	33.8	4.4	166094	2	BX469905	BX469905 Danio rer	C 798	33.6	4.4	12388	9	AY043326	AY043326 Homo sapi
C 726	33.8	4.4	169879	2	AC073144	AC073144 Homo sapi	799	33.6	4.4	14488	1	AE005355	AE005355 Escherich
C 727	33.8	4.4	170756	5	BX248508	BX248508 Zebrafish	C 800	33.6	4.4	17970	6	AX458517	AX458517 Sequence
728	33.8	4.4	171076	2	AC024409	AC024409 Homo sapi	C 801	33.6	4.4	37658	2	AC149362	AC149362 Phakopsor
729	33.8	4.4	171345	9	CNS01RII	AL163612 Human chr	802	33.6	4.4	40275	9	AY500996	AY500996 Homo sapi
C 730	33.8	4.4	172281	8	AC134046	AC134046 Oryza sat	C 803	33.6	4.4	65720	2	AC091037	AC091037 Homo sapi
731	33.8	4.4	172765	5	BX842701	BX842701 Zebrafish	804	33.6	4.4	103000	2	AC008727	AC008727 Homo sapi
C 732	33.8	4.4	172989	10	AC131112	AC131112 Mus muscu	C 805	33.6	4.4	104081	9	HSDJ263J7	AL049545 Human DNA
C 733	33.8	4.4	173805	2	AL606966	AL606966 Homo sapi	806	33.6	4.4	105618	8	AC148340	AC148340 Medicago
734	33.8	4.4	177076	2	AC092949	AC092949 Homo sapi	807	33.6	4.4	106277	9	AC068792	AC068792 Homo sapi
735	33.8	4.4	177127	2	AC026287	AC026287 Homo sapi	C 808	33.6	4.4	108265	9	AL133547	AL133547 Human DNA
736	33.8	4.4	177174	2	AC120281	AC120281 Rattus no	C 809	33.6	4.4	110000	2	BX004982_0	BX004982 Homo sapi
737	33.8	4.4	177664	2	AC015749	AC015749 Homo sapi	C 810	33.6	4.4	110000	9	AF440620_1	Continuation (2 of
738	33.8	4.4	181352	2	AC101973	AC101973 Mus muscu	C 811	33.6	4.4	112080	9	HS482L13	AL031446 Human DNA
C 739	33.8	4.4	181430	2	AC123713	AC123713 Mus muscu	C 812	33.6	4.4	114367	8	ATF10M10	AL035521 Arabidops
C 740	33.8	4.4	182115	2	AC133898	AC133898 Mus muscu	C 813	33.6	4.4	117349	9	HSJ1060K6	AL049690 Human DNA
741	33.8	4.4	183357	9	AC068759	AC068759 Homo sapi	C 814	33.6	4.4	117406	2	OSJN002L1	AL663010 Oryza sat
C 742	33.8	4.4	184892	10	AC016017	AC016017 Mus Muscu	815	33.6	4.4	121682	2	AL139127	AL139127 Homo sapi
C 743	33.8	4.4	185944	2	AC119975	AC119975 Mus muscu	816	33.6	4.4	121995	2	AC091512	AC091512 Leishmani
C 744	33.8	4.4	188923	9	AC026802	AC026802 Homo sapi	C 817	33.6	4.4	123209	9	AL158195	AL158195 Human DNA
745	33.8	4.4	189104	10	AL806522	AL806522 Mouse DNA	C 818	33.6	4.4	125661	9	AL138773	AL138773 Human DNA
746	33.8	4.4	189115	2	AC107680	AC107680 Mus muscu	C 819	33.6	4.4	126951	2	AC110181	AC110181 Mus muscu
747	33.8	4.4	189834	2	AC132696	AC132696 Rattus no	C 820	33.6	4.4	136006	9	AC006151	AC006151 Homo sapi
748	33.8	4.4	191578	10	AC099591	AC099591 Mus muscu	C 821	33.6	4.4	136225	9	AC004860	AC004860 Homo sapi
749	33.8	4.4	192967	2	AC148895	AC148895 Otolemur	C 822	33.6	4.4	139727	10	AC125680	AC125680 Rattus no

823	33.6	4.4	143107	9	AC005949	AC005949 Homo sapi
824	33.6	4.4	143549	2	AP003910	AP003910 Oryza sat
825	33.6	4.4	145652	10	AL929262	AL929262 Mouse DNA
826	33.6	4.4	148900	2	AC025404	AC025404 Homo sapi
827	33.6	4.4	151046	8	AP004566	AP004566 Oryza sat
828	33.6	4.4	151162	2	AC025601	AC025601 Homo sapi
829	33.6	4.4	154084	9	AC022311	AC022311 Homo sapi
830	33.6	4.4	154284	10	AC005992	AC005992 Mus muscu
831	33.6	4.4	157000	2	AC026511	AC026511 Homo sapi
832	33.6	4.4	161633	2	AL592288	AL592288 Homo sapi
833	33.6	4.4	161815	9	AC092015	AC092015 Homo sapi
834	33.6	4.4	167758	2	AC068746	AC068746 Homo sapi
835	33.6	4.4	168672	2	AC024920	AC024920 Homo sapi
836	33.6	4.4	169557	9	AC024706	AC024706 Homo sapi
837	33.6	4.4	170849	9	AC126366	AC126366 Homo sapi
838	33.6	4.4	171451	2	AC064838	AC064838 Homo sapi
839	33.6	4.4	173308	9	HS859D4	AL035668 Human DNA
840	33.6	4.4	178975	2	AC109974	AC109974 Rattus no
841	33.6	4.4	179350	9	AC026351	AC026351 Homo sapi
842	33.6	4.4	179503	9	AL445468	AL445468 Human DNA
843	33.6	4.4	181433	9	CNS00006	AL049775 Human chr
844	33.6	4.4	181527	10	AC140788	AC140788 Mus muscu
845	33.6	4.4	182207	2	AC109242	AC109242 Mus muscu
846	33.6	4.4	182934	5	BX000690	BX000690 Zebrafish
847	33.6	4.4	190842	9	AC004885	AC004885 Homo sapi
848	33.6	4.4	191947	9	AC107016	AC107016 Homo sapi
849	33.6	4.4	194770	2	AL149064	AL149064 Homo sapi
850	33.6	4.4	195921	8	ATCHRIV81	AL161585 Arabidops
851	33.6	4.4	197964	9	AC079904	AC079904 Homo sapi
852	33.6	4.4	198564	9	AC008581	AC008581 Homo sapi
853	33.6	4.4	200097	2	AC129104	AC129104 Homo sapi
854	33.6	4.4	202815	9	AF267169	AF267169 Homo sapi
855	33.6	4.4	206790	10	AC123608	AC123608 Mus muscu
856	33.6	4.4	207346	10	BX255938	BX255938 Mouse DNA
857	33.6	4.4	207699	2	BX470159	BX470159 Danio rer
858	33.6	4.4	209196	2	AC017024	AC017024 Homo sapi
859	33.6	4.4	211296	10	AC113059	AC113059 Mus muscu
860	33.6	4.4	213223	2	CR376855	CR376855 Danio rer
861	33.6	4.4	216726	2	AC097270	AC097270 Pan trogl
862	33.6	4.4	221537	2	AC117664	AC117664 Mus muscu
863	33.6	4.4	236761	2	AC103282	AC103282 Rattus no
864	33.6	4.4	237468	2	AC108532	AC108532 Rattus no
865	33.6	4.4	241956	2	BX323393	BX323393 Mus muscu
866	33.6	4.4	243329	5	AC145979	AC145979 Gallus ga
867	33.6	4.4	246612	2	AC008579	AC008579 Homo sapi
868	33.6	4.4	246890	2	AC117302	AC117302 Rattus no
869	33.6	4.4	250096	10	AC107773	AC107773 Mus muscu
870	33.6	4.4	254594	2	AC132698	AC132698 Rattus no
871	33.6	4.4	261825	2	AC106351	AC106351 Rattus no
872	33.6	4.4	264410	10	AC116119	AC116119 Mus muscu
873	33.6	4.4	286485	1	AP002557	AP002557 Escherich
874	33.6	4.4	295788	2	AC109126	AC109126 Rattus no
875	33.6	4.4	308232	2	AL392004	AL392004 Homo sapi
876	33.6	4.4	310122	2	AC126797	AC126797 Mus muscu
877	33.6	4.4	319367	10	AC021709	AC021709 Mus muscu
878	33.4	4.4	400	10	MMXWV9	Z46250 M.musculus
879	33.4	4.4	626	11	G58719	G58719 SHGC-105512
880	33.4	4.4	912	6	CQ646832	CQ646832 Sequence
881	33.4	4.4	918	10	AY318209	AY318209 Mus muscu
882	33.4	4.4	1572	8	AK117417	AK117417 Arabidops
883	33.4	4.4	2031	9	AB050429	AB050429 Macaca fa
884	33.4	4.4	5975	6	AX251790	AX251790 Sequence
885	33.4	4.4	6558	6	CQ806878	CQ806878 Sequence
886	33.4	4.4	6558	6	CQ807152	CQ807152 Sequence
887	33.4	4.4	6558	6	AX251304	AX251304 Sequence
888	33.4	4.4	6558	6	AX795814	AX795814 Sequence
889	33.4	4.4	6558	6	AX795930	AX795930 Sequence
890	33.4	4.4	6558	6	AX822324	AX822324 Sequence
891	33.4	4.4	6558	6	AX822452	AX822452 Sequence
892	33.4	4.4	6558	6	AX825964	AX825964 Sequence
893	33.4	4.4	6558	6	AX826092	AX826092 Sequence
894	33.4	4.4	9640	9	AC093375	AC093375 Homo sapi
895	33.4	4.4	10001	6	CQ807039	CQ807039 Sequence

896	33.4	4.4	10001	6	CQ807313	CQ807313 Sequence
897	33.4	4.4	11049	1	AE006530	AE006530 Streptoco
898	33.4	4.4	14186	5	XBUT15XB	Z54313 X.borealis
899	33.4	4.4	16967	3	AB055624	AB055624 Inverse
900	33.4	4.4	17308	10	AL929285	AL929285 Mouse DNA
901	33.4	4.4	23907	3	U61951	U61951 Caenorhabdi
902	33.4	4.4	34990	2	AC022112	AC022112 Homo sapi
903	33.4	4.4	38740	9	HSU59962	U59962 Human cosmi
904	33.4	4.4	40600	3	CEF20D1	Z78542 Caenorhabdi
905	33.4	4.4	41618	9	AL355473	AL355473 Human DNA
906	33.4	4.4	51719	1	AE014147	AE014147 Streptoco
907	33.4	4.4	58366	6	AX647879	AX647879 Sequence
908	33.4	4.4	65521	2	AC101449	AC101449 Mus muscu
909	33.4	4.4	71953	8	AB081587	AB081587 Prunus du
910	33.4	4.4	79834	9	AP000948	AP000948 Homo sapi
911	33.4	4.4	81699	10	AL713925	AL713925 Mouse DNA
912	33.4	4.4	93301	2	AC074165	AC074165 Mus muscu
913	33.4	4.4	97805	2	AC074157	AC074157 Mus muscu
914	33.4	4.4	97805	2	AC074157	AC074157 Mus muscu
915	33.4	4.4	102375	2	AC025042	AC025042 Homo sapi
916	33.4	4.4	105736	10	AL772359	AL772359 Mouse DNA
917	33.4	4.4	108112	5	BX470170	BX470170 Zebrafish
918	33.4	4.4	108189	9	AC007128	AC007128 Homo sapi
919	33.4	4.4	110000	1	CP000003_06	Continuation (7 of
920	33.4	4.4	110000	2	AC109620_0	AC109620 Mus muscu
921	33.4	4.4	110000	2	BX294172_1	Continuation (2 of
922	33.4	4.4	112070	9	AC068798	AC068798 Homo sapi
923	33.4	4.4	113937	8	AC143338	AC143338 Medicago
924	33.4	4.4	115040	8	AC124954	AC124954 Medicago
925	33.4	4.4	123988	9	HSJ914M10	AL121763 Human DNA
926	33.4	4.4	124964	9	AL159154	AL159154 Human DNA
927	33.4	4.4	138257	2	AC149471	AC149471 Medicago
928	33.4	4.4	138627	9	AC099500	AC099500 Homo sapi
929	33.4	4.4	143092	2	AC051641	AC051641 Homo sapi
930	33.4	4.4	147874	2	AC011278	AC011278 Homo sapi
931	33.4	4.4	149848	2	AC119516	AC119516 Rattus no
932	33.4	4.4	150438	9	AC099517	AC099517 Homo sapi
933	33.4	4.4	151225	9	AC012625	AC012625 Homo sapi
934	33.4	4.4	156492	2	AC008460	AC008460 Homo sapi
935	33.4	4.4	158907	9	AC011890	AC011890 Homo sapi
936	33.4	4.4	160558	2	AC025832	AC025832 Homo sapi
937	33.4	4.4	160708	2	AC011962	AC011962 Homo sapi
938	33.4	4.4	162417	10	AC102769	AC102769 Mus muscu
939	33.4	4.4	163823	9	AC097372	AC097372 Homo sapi
940	33.4	4.4	164647	9	AC080183	AC080183 Homo sapi
941	33.4	4.4	165965	2	AC012287	AC012287 Homo sapi
942	33.4	4.4	167248	10	AC141885	AC141885 Mus muscu
943	33.4	4.4	167493	5	BX322607	BX322607 Zebrafish
944	33.4	4.4	169500	2	AC138469	AC138469 Homo sapi
945	33.4	4.4	169693	9	HS57A13	Z83848 Human DNA s
946	33.4	4.4	169830	2	AC013345	AC013345 Homo sapi
947	33.4	4.4	170916	9	AL136300	AL136300 Human DNA
948	33.4	4.4	171593	10	AL672074	AL672074 Mouse DNA
949	33.4	4.4	172314	2	AC026154	AC026154 Homo sapi
950	33.4	4.4	174383	2	AC012053	AC012053 Homo sapi
951	33.4	4.4	175179	10	AC134560	AC134560 Mus muscu
952	33.4	4.4	178660	9	HSG1150	AJ006996 Homo sapi
953	33.4	4.4	179762	2	AC013519	AC013519 Homo sapi
954	33.4	4.4	180885	2	AC110252	AC110252 Mus muscu
955	33.4	4.4	180944	9	AC084855	AC084855 Homo sapi
956	33.4	4.4	182147	9	AC062032	AC062032 Homo sapi
957	33.4	4.4	183761	2	AC120450	AC120450 Rattus no
958	33.4	4.4	185581	10	AC132244	AC132244 Mus muscu
959	33.4	4.4	188735	10	AC111091	AC111091 Mus muscu
960	33.4	4.4	189236	10	AL607030	AL607030 Mouse DNA
961	33.4	4.4	192641	5	BX322588	BX322588 Zebrafish
962	33.4	4.4	193423	2	BX571851	BX571851 Danio rer
963	33.4	4.4	193963	9	AC013475	AC013475 Homo sapi
964	33.4	4.4	195880	2	AC149277	AC149277 Mus muscu
965	33.4	4.4	199917	2	AC006755	AC006755 Caenorhab
966	33.4	4.4	200461	9	AL592402	AL592402 Human DNA
967	33.4	4.4	204590	10	AC124738	AC124738 Mus muscu
968	33.4	4.4	208922	5	AL929017	AL929017 Zebrafish

969	33.4	4.4	208942	2	AC121011	AC121011 Rattus no	c1042	33.2	4.3	166354	2	AL929579	AL929579 Danio rer
970	33.4	4.4	211986	5	BX511229	BX511229 Zebrafish	c1043	33.2	4.3	166870	2	BX927276	BX927276 Danio rer
971	33.4	4.4	212074	2	AC127787	AC127787 Rattus no	1044	33.2	4.3	167181	2	AC131701	AC131701 Mus muscu
C 972	33.4	4.4	213589	2	AC097281	AC097281 Rattus no	c1045	33.2	4.3	168605	2	AC022477	AC022477 Homo sapi
973	33.4	4.4	214779	2	AC112769	AC112769 Rattus no	c1046	33.2	4.3	170022	9	AC024367	AC024367 Homo sapi
974	33.4	4.4	221733	2	AC128906	AC128906 Rattus no	1047	33.2	4.3	172350	2	AC079234	AC079234 Homo sapi
975	33.4	4.4	221813	2	AC116707	AC116707 Mus muscu	1048	33.2	4.3	174098	9	AC005737	AC005737 Homo sapi
C 976	33.4	4.4	222940	2	AC097839	AC097839 Rattus no	1049	33.2	4.3	175161	2	BX927396	BX927396 Danio rer
C 977	33.4	4.4	223808	2	AC114139	AC114139 Rattus no	1050	33.2	4.3	176470	9	AL353626	AL353626 Human DNA
C 978	33.4	4.4	227022	2	AC149933	AC149933 Strongylo	1051	33.2	4.3	176473	2	AC090986	AC090986 Homo sapi
979	33.4	4.4	230155	2	AC114073	AC114073 Rattus no	1052	33.2	4.3	176642	10	AC121987	AC121987 Mus muscu
C 980	33.4	4.4	231200	2	AC113399	AC113399 Homo sapi	c1053	33.2	4.3	176981	2	AC130261	AC130261 Rattus no
C 981	33.4	4.4	232092	2	AC127800	AC127800 Rattus no	1054	33.2	4.3	178387	10	AC121928	AC121928 Mus muscu
982	33.4	4.4	232877	2	AC094618	AC094618 Rattus no	1055	33.2	4.3	178704	9	BX119904	BX119904 Human DNA
C 983	33.4	4.4	233796	2	AC130568	AC130568 Rattus no	c1056	33.2	4.3	178824	9	AC146421	AC146421 Pan trogl
C 984	33.4	4.4	237732	2	AC127135	AC127135 Rattus no	c1057	33.2	4.3	181413	9	AC080032	AC080032 Homo sapi
985	33.4	4.4	238934	2	BX548160	BX548160 Danio rer	c1058	33.2	4.3	182997	9	AL355332	AL355332 Human DNA
986	33.4	4.4	240539	2	BX571803	BX571803 Danio rer	c1059	33.2	4.3	183052	2	AC109892	AC109892 Rattus no
C 987	33.4	4.4	241036	2	AC095383	AC095383 Rattus no	1060	33.2	4.3	183946	2	AC009164	AC009164 Homo sapi
C 988	33.4	4.4	248466	2	AC105146	AC105146 Plasmodi	c1061	33.2	4.3	184144	9	AL451010	AL451010 Human DNA
C 989	33.4	4.4	249995	3	AE014840	AE014840 Plasmodi	c1062	33.2	4.3	189589	2	AC146641	AC146641 Otolemur
C 990	33.4	4.4	253918	2	AC106931	AC106931 Rattus no	c1063	33.2	4.3	190806	2	AC115436	AC115436 Rattus no
C 991	33.4	4.4	256635	2	AC128838	AC128838 Rattus no	c1064	33.2	4.3	191046	10	AL607146	AL607146 Mouse DNA
C 992	33.4	4.4	257518	2	AC118524	AC118524 Rattus no	c1065	33.2	4.3	191684	2	AC018826	AC018826 Homo sapi
993	33.4	4.4	260286	2	AC129651	AC129651 Rattus no	c1066	33.2	4.3	191713	10	AC124397	AC124397 Mus muscu
C 994	33.4	4.4	270264	2	AC103092	AC103092 Rattus no	c1067	33.2	4.3	191964	2	AC119311	AC119311 Rattus no
C 995	33.4	4.4	276343	2	AC125570	AC125570 Rattus no	c1068	33.2	4.3	194160	2	AC131911	AC131911 Mus muscu
996	33.4	4.4	300029	1	AE017297	AE017297 Leptospi	1069	33.2	4.3	194372	9	AC019184	AC019184 Homo sapi
C 997	33.4	4.4	340000	9	AP001691	AP001691 Homo sapi	1070	33.2	4.3	194551	9	AC092291	AC092291 Homo sapi
C 998	33.4	4.4	340000	9	AP001700	AP001700 Homo sapi	1071	33.2	4.3	194892	2	CR376797	CR376797 Danio rer
C 999	33.4	4.4	340000	9	HS21C046	AL163246 Homo sapi	c1072	33.2	4.3	195057	2	CR381708	CR381708 Danio rer
c1000	33.2	4.3	519	11	G59093	G59093 SHGC-106668	c1073	33.2	4.3	196009	5	BX548045	BX548045 Zebrafish
c1001	33.2	4.3	564	11	G58955	G58955 SHGC-106725	1074	33.2	4.3	197139	2	AC141894	AC141894 Mus muscu
c1002	33.2	4.3	1055	6	AX083745	AX083745 Sequence	c1075	33.2	4.3	198430	5	BX664716	BX664716 Zebrafish
1003	33.2	4.3	13286	6	CQ807296	CQ807296 Sequence	c1076	33.2	4.3	198949	9	AC010287	AC010287 Homo sapi
1004	33.2	4.3	30849	3	AC117082	AC117082 Dictyoste	1077	33.2	4.3	199287	2	AC068659	AC068659 Homo sapi
1005	33.2	4.3	38240	3	CEB0491	Z49907 Caenorhabdi	c1078	33.2	4.3	201567	9	AC011901	AC011901 Homo sapi
1006	33.2	4.3	38262	9	HSN98E6	Z68325 Human DNA s	c1079	33.2	4.3	202563	2	AC102479	AC102479 Mus muscu
c1007	33.2	4.3	47756	2	AC136356	AC136356 Homo sapi	1080	33.2	4.3	205562	2	AC126511	AC126511 Rattus no
1008	33.2	4.3	72751	9	AC090112	AC090112 Pan trogl	c1081	33.2	4.3	207906	2	BX927226	BX927226 Danio rer
c1009	33.2	4.3	93826	8	AC108876	AC108876 Oryza sat	1082	33.2	4.3	209243	2	BX119920	BX119920 Danio rer
c1010	33.2	4.3	95455	5	BX324232	BX324232 Zebrafish	1083	33.2	4.3	220173	9	AC012183	AC012183 Homo sapi
c1011	33.2	4.3	114802	9	AC026230	AC026230 Homo sapi	c1084	33.2	4.3	220832	2	AC126145	AC126145 Rattus no
1012	33.2	4.3	122049	5	BX649332	BX649332 Zebrafish	c1085	33.2	4.3	222284	2	AC024442	AC024442 Homo sapi
1013	33.2	4.3	127058	2	AC025652	AC025652 Homo sapi	1086	33.2	4.3	222728	2	AC141289	AC141289 Homo sapi
c1014	33.2	4.3	130088	9	AC110073	AC110073 Homo sapi	1087	33.2	4.3	223182	5	AL929049	AL929049 Zebrafish
c1015	33.2	4.3	132029	9	HS795G23	AL031000 Human DNA	c1088	33.2	4.3	223306	10	AC125181	AC125181 Mus muscu
c1016	33.2	4.3	135224	2	AC022373	AC022373 Homo sapi	1089	33.2	4.3	225880	2	AC131693	AC131693 Mus muscu
1017	33.2	4.3	136064	10	AL928992	AL928992 Mouse DNA	c1090	33.2	4.3	226735	2	AC121120	AC121120 Mus muscu
1018	33.2	4.3	138710	10	AC023608	AC023608 Mus muscu	c1091	33.2	4.3	226837	2	AC142476	AC142476 Rattus no
1019	33.2	4.3	143428	9	AL162587	AL162587 Human DNA	1092	33.2	4.3	231303	2	BX649405	BX649405 Danio rer
1020	33.2	4.3	143741	10	BX001009	BX001009 Mouse DNA	c1093	33.2	4.3	231868	2	AC118124	AC118124 Rattus no
1021	33.2	4.3	144084	2	BX571682	BX571682 Danio rer	c1094	33.2	4.3	238379	2	AL590986	AL590986 Homo sapi
1022	33.2	4.3	148851	9	HS155D22	Z97205 Human DNA s	c1095	33.2	4.3	244574	2	AC103190	AC103190 Rattus no
1023	33.2	4.3	149818	2	AC105955	AC105955 Mus muscu	1096	33.2	4.3	245717	2	AC136281	AC136281 Rattus no
1024	33.2	4.3	151802	3	AC114263	AC114263 Dictyoste	1097	33.2	4.3	249684	2	AC132983	AC132983 Rattus no
c1025	33.2	4.3	152158	2	BX649301	BX649301 Danio rer	1098	33.2	4.3	252614	5	BX255907	BX255907 Zebrafish
c1026	33.2	4.3	152181	9	AL391869	AL391869 Human DNA	1099	33.2	4.3	255917	2	AC112350	AC112350 Rattus no
c1027	33.2	4.3	152706	5	AL935302	AL935302 Zebrafish	c1100	33.2	4.3	258373	2	AC093995	AC093995 Rattus no
1028	33.2	4.3	153495	2	AC115841	AC115841 Mus muscu	1101	33.2	4.3	263789	2	AC103242	AC103242 Rattus no
1029	33.2	4.3	154085	2	BX537124	BX537124 Danio rer	c1102	33.2	4.3	266237	2	AC094800	AC094800 Rattus no
c1030	33.2	4.3	155540	5	BX324162	BX324162 Zebrafish	1103	33.2	4.3	277858	2	AC113643	AC113643 Rattus no
1031	33.2	4.3	157583	5	BX571951	BX571951 Zebrafish	c1104	33.2	4.3	300794	8	AE016884	AE016884 Erethothec
1032	33.2	4.3	158327	2	BX927212	BX927212 Danio rer	1105	33.2	4.3	308918	2	AC128085	AC128085 Rattus no
c1033	33.2	4.3	158806	2	AL591132	AL591132 Homo sapi	1106	33.2	4.3	314016	2	AC146012	AC146012 Pan trogl
c1034	33.2	4.3	158963	2	AC141725	AC141725 Apis mell	1107	33.2	4.3	320398	2	AC136192	AC136192 Rattus no
1035	33.2	4.3	159941	10	AC125354	AC125354 Mus muscu	1108	33.2	4.3	341050	3	PFA929357	AL929357 Plasmodi
1036	33.2	4.3	160077	2	AC149568	AC149568 Papio anu	1109	33.2	4.3	349980	6	AX344556	AX344556 Sequence
c1037	33.2	4.3	164006	9	BX000449	BX000449 Human DNA	1110	33	4.3	304	6	CQ698694	CQ698694 Sequence
1038	33.2	4.3	164508	2	AC104130	AC104130 Homo sapi	1111	33	4.3	614	11	BV160444	BV160444 RPAMSEQO
1039	33.2	4.3	165062	9	AC087834	AC087834 Pan trogl	c1112	33	4.3	1010	8	AF159385	AF159385 Hordeum b
c1040	33.2	4.3	165695	2	CR352250	CR352250 Danio rer	1113	33	4.3	1078	3	AY368909	AY368909 Synergus
1041	33.2	4.3	166253	9	AC008900	AC008900 Homo sapi	1114	33	4.3	1227	10	RNO250730	RNO250730 Rattus no

c1115 4.3 1391 6 AX878715 Sequence
c1116 4.3 1391 6 BD157402 Primer fo
c1117 4.3 1391 9 AK021832 Homo sapi
c1118 4.3 1581 8 AF441395 Candida a
c1119 4.3 1602 6 AX506162 Sequence
c1120 4.3 1683 8 AY081532 Arabidops
c1121 4.3 1763 8 AY054633 Arabidops
c1122 4.3 1908 8 ATH305961 Arabidops
c1123 4.3 2000 6 AX655393 Sequence
c1124 4.3 3103 1 AF269420 Staphyloc
c1125 4.3 3103 6 AR485376 Sequence
c1126 4.3 3103 6 AX144740 Sequence
c1127 4.3 3438 1 AF270201 Staphyloc
c1128 4.3 3438 6 AR486155 Sequence
c1129 4.3 3438 6 AX145519 Sequence
c1130 4.3 3463 1 AF269957 Staphyloc
c1131 4.3 3463 6 AR485911 Sequence
c1132 4.3 3463 6 AX145275 Sequence
c1133 4.3 4578 9 BC038296 Homo sapi
c1134 4.3 7276 10 AL732549 Mouse DNA
c1135 4.3 9263 6 CQ592241 Sequence
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c1137 4.3 21460 9 AL589927 Human DNA
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c1145 4.3 85980 5 AL591671 Homo sapi
c1146 4.3 90963 9 AC012602 Homo sapi
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c1149 4.3 105468 8 AP004852 Oryza sat
c1150 4.3 110000 2 AC101662 Mus muscu
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c1152 4.3 119119 9 AC008970 Homo sapi
c1153 4.3 120548 3 AC024798 Caenorhab
c1154 4.3 125566 2 AC069447 Mus muscu
c1155 4.3 125729 6 AX818232 Sequence
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c1166 4.3 149724 4 AC129888 Atelexir
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c1168 4.3 158921 9 AC024329 Homo sapi
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c1184 4.3 177806 9 AC093106 Homo sapi
c1185 4.3 177921 2 AC112343 Rattus no
c1186 4.3 178553 2 AC006891 Caenorhab
c1187 4.3 178965 3 AC010117 Drosophil

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4.3 179055 3 AC093551 Drosophil
4.3 179839 3 AC022342 Drosophil
4.3 184547 9 AC011626 Homo sapi
4.3 184716 2 AC026492 Mus muscu
4.3 185799 2 CR381553 Danio rer
4.3 186279 10 AC121977 Mus muscu
4.3 187533 5 BX950191 Zebrafish
4.3 193250 9 AC027238 Homo sapi
4.3 195621 2 AC133060 Rattus no
4.3 195771 2 AC091692 Homo sapi
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4.3 196452 2 AC018869 Homo sapi
4.3 199131 2 AC027325 Homo sapi
4.3 199956 10 AC147241 Mus muscu
4.3 202228 2 AC124646 Mus muscu
4.3 202521 2 AC146953 Pongo pyg
4.3 203058 5 AL844150 Zebrafish
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4.3 205816 2 AC145411 Bos tauru
4.3 206616 2 CNS00M8U Homo sapi
4.3 206837 10 AC124733 Mus muscu
4.3 208961 2 AC125450 Mus muscu
4.3 214520 2 AC125256 Mus muscu
4.3 214678 2 CR388060 Danio rer
4.3 217073 2 AC114144 Rattus no
4.3 218023 2 AC115925 Mus muscu
4.3 220874 2 CR376848 Danio rer
4.3 222938 2 AC095075 Rattus no
4.3 224144 2 AC107714 Mus muscu
4.3 224802 2 AC006787 Caenorhab
4.3 226225 2 AC121002 Rattus no
4.3 227993 10 AL645930 Mouse DNA
4.3 230685 2 AC131318 Mus muscu
4.3 237992 2 AC102617 Mus muscu
4.3 240729 2 AC111961 Rattus no
4.3 241498 10 AC109168 Mus muscu
4.3 244435 2 AC098137 Rattus no
4.3 245156 2 AC084021 Mus muscu
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4.3 249281 2 AC095277 Rattus no
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4.3 252146 2 AC118155 Rattus no
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4.3 259871 2 AC107164 Rattus no
4.3 260987 2 AC121031 Rattus no
4.3 280115 2 AC105710 Rattus no
4.3 282895 2 AL133478 Homo sapi
4.3 293161 2 BX908750 Danio rer
4.3 295920 2 AC108611 Rattus no
4.3 300787 1 AE016744 Staphyloc
4.3 314896 2 AC091357 Rattus no
4.3 315098 3 AE003495 Drosophil
4.3 322554 3 AE003592 Drosophil
4.3 336376 2 AC106127 Rattus no
4.3 387 10 RN059800 U59800 Rattus norv
4.3 408 6 AX300942 Sequence
4.3 685 11 G56885 SHGC-102618
4.3 807 11 BV154605 ESRI_43 R
4.3 7546 1 AY082011 Enterococ
4.3 9010 14 AF178440 Triatoma
4.3 11173 9 AC126173 Homo sapi
4.3 11181 9 AC128679 Homo sapi
4.3 15361 4 OCCR
4.3 15823 4 OCRYAN
4.3 38194 5 BX571725 Carp DNA
4.3 38589 9 AC068994 Homo sapi
4.3 39210 3 U41508 Caenorhabdi
4.3 45434 10 AL805979 Mouse DNA
4.3 47268 2 AC020414 Drosophil
4.3 58972 2 AC137725 Mus muscu
4.3 63601 9 AC080135 Homo sapi

1261	32.8	4.3	72143	2	AC016006	AC016006 Homo sapi
1262	32.8	4.3	72751	9	AC090112	AC090112 Pan trogl
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1265	32.8	4.3	90479	2	AC121463_3	Continuation (4 of
1266	32.8	4.3	91570	8	ATT13K14	AL080282 Arabidops
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1269	32.8	4.3	110000	1	AE017355_22	Continuation (23 o
1270	32.8	4.3	110000	1	AE017355_27	Continuation (28 o
1271	32.8	4.3	110000	10	AE014180_2	Continuation (3 of
1272	32.8	4.3	112155	8	CR378661	CR378661 M.truncat
1273	32.8	4.3	116351	8	AP005574	AP005574 Oryza sat
1274	32.8	4.3	120366	10	AL845531	AL845531 Mouse DNA
1275	32.8	4.3	120761	8	AC124218	AC124218 Medicago
1276	32.8	4.3	121055	8	AC122144	AC122144 Oryza sat
1277	32.8	4.3	125425	10	AC102845	AC102845 Mus muscu
1278	32.8	4.3	132249	2	AC142362	AC142362 Rattus no
1279	32.8	4.3	136493	2	AC125500	AC125500 Takifugu
1280	32.8	4.3	138640	2	AC128217	AC128217 Rattus no
1281	32.8	4.3	139874	8	AP005522	AP005522 Oryza sat
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1283	32.8	4.3	144252	8	AP005399	AP005399 Oryza sat
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1285	32.8	4.3	145042	10	AL732425	AL732425 Mouse DNA
1286	32.8	4.3	148208	2	AC010951	AC010951 Homo sapi
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1288	32.8	4.3	151348	9	AC087713	AC087713 Homo sapi
1289	32.8	4.3	152432	2	AC025746	AC025746 Homo sapi
1290	32.8	4.3	154356	10	AC131119	AC131119 Mus muscu
1291	32.8	4.3	155150	9	AC015542	AC015542 Homo sapi
1292	32.8	4.3	159082	2	AC145257	AC145257 Felis cat
1293	32.8	4.3	159532	2	AC118446	AC118446 Rattus no
1294	32.8	4.3	161434	2	AL138817	AL138817 Homo sapi
1295	32.8	4.3	162246	10	BX000428	BX000428 Mouse DNA
1296	32.8	4.3	162808	2	AC021340	AC021340 Homo sapi
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1298	32.8	4.3	164297	2	AC012138	AC012138 Homo sapi
1299	32.8	4.3	164500	2	AC069171	AC069171 Homo sapi
1300	32.8	4.3	164655	2	AC080134	AC080134 Homo sapi
1301	32.8	4.3	165136	3	AC007645	AC007645 Drosophil
1302	32.8	4.3	165197	9	HSAC002070	AC002070 Human BAC
1303	32.8	4.3	165940	2	AC103602	AC103602 Mus muscu
1304	32.8	4.3	165940	9	AC068112	AC068112 Homo sapi
1305	32.8	4.3	167108	9	CNS01RHA	AL161666 Human chr
1306	32.8	4.3	167710	2	AC109891	AC109891 Rattus no
1307	32.8	4.3	167881	2	AC079909	AC079909 Homo sapi
1308	32.8	4.3	167921	9	AL392110	AL392110 Human DNA
1309	32.8	4.3	168111	9	HS525L6	AL023807 Human DNA
1310	32.8	4.3	168790	5	BX571842	BX571842 Zebrafish
1311	32.8	4.3	168858	10	AC124429	AC124429 Mus muscu
1312	32.8	4.3	168946	2	BX664731	BX664731 Danio rer
1313	32.8	4.3	169199	9	AC090497	AC090497 Homo sapi
1314	32.8	4.3	170121	9	AF064860	AF064860 Homo sapi
1315	32.8	4.3	171523	9	AC010206	AC010206 Homo sapi
1316	32.8	4.3	173153	9	AC008119	AC008119 Homo sapi
1317	32.8	4.3	173217	2	CR457448	CR457448 Danio rer
1318	32.8	4.3	174910	8	AC137002	AC137002 Oryza sat
1319	32.8	4.3	176261	8	AP003274	AP003274 Oryza sat
1320	32.8	4.3	177565	8	AC092388	AC092388 Oryza sat
1321	32.8	4.3	177967	10	AC122816	AC122816 Mus muscu
1322	32.8	4.3	178620	10	AC121865	AC121865 Mus muscu
1323	32.8	4.3	178824	9	AC146421	AC146421 Pan trogl
1324	32.8	4.3	179953	2	BX927407	BX927407 Danio rer
1325	32.8	4.3	181609	9	AC079385	AC079385 Homo sapi
1326	32.8	4.3	181804	9	AC107068	AC107068 Homo sapi
1327	32.8	4.3	183075	5	AC145959	AC145959 Gallus ga
1328	32.8	4.3	183597	9	AL356285	AL356285 Human DNA
1329	32.8	4.3	183815	9	AL451084	AL451084 Human DNA
1330	32.8	4.3	185212	2	BX572088	BX572088 Mus muscu
1331	32.8	4.3	188676	2	AC024515	AC024515 Homo sapi
1332	32.8	4.3	189932	2	AC146117	AC146117 Pan trogl
1333	32.8	4.3	192020	10	AC140303	AC140303 Mus muscu

1334	32.8	4.3	194068	2	AC115327	AC115327 Rattus no
1335	32.8	4.3	194387	10	AC105989	AC105989 Mus muscu
1336	32.8	4.3	196248	5	AL845328	AL845328 Zebrafish
1337	32.8	4.3	197024	2	CR513789	CR513789 Danio rer
1338	32.8	4.3	197568	8	ATCHRIV53	AL161553 Arabidops
1339	32.8	4.3	197782	9	AC012377	AC012377 Homo sapi
1340	32.8	4.3	198715	8	ATCHRIV54	AL161554 Arabidops
1341	32.8	4.3	199259	10	AC074313	AC074313 Mus muscu
1342	32.8	4.3	200000	2	AC006294	AC006294 Homo sapi
1343	32.8	4.3	201620	2	AC109278	AC109278 Mus muscu
1344	32.8	4.3	202342	10	AC139063	AC139063 Mus muscu
1345	32.8	4.3	202561	2	AC126479	AC126479 Rattus no
1346	32.8	4.3	202565	9	AL354696	AL354696 Human DNA
1347	32.8	4.3	203047	10	AC127289	AC127289 Mus muscu
1348	32.8	4.3	203993	2	AC134867	AC134867 Mus muscu
1349	32.8	4.3	207430	10	AL772236	AL772236 Mouse DNA
1350	32.8	4.3	209405	2	BX901887	BX901887 Danio rer
1351	32.8	4.3	209618	10	AC125688	AC125688 Rattus no
1352	32.8	4.3	209894	2	AC098267	AC098267 Rattus no
1353	32.8	4.3	210298	3	AE003690	AE003690 Drosophil
1354	32.8	4.3	213335	2	AC141961	AC141961 Rattus no
1355	32.8	4.3	213401	2	AC124940	AC124940 Rattus no
1356	32.8	4.3	213865	9	AC093166	AC093166 Homo sapi
1357	32.8	4.3	218262	2	AC105870	AC105870 Rattus no
1358	32.8	4.3	231313	2	CR354535	CR354535 Danio rer
1359	32.8	4.3	231980	2	AC094305	AC094305 Rattus no
1360	32.8	4.3	233549	2	AC137326	AC137326 Rattus no
1361	32.8	4.3	235717	2	AC127918	AC127918 Rattus no
1362	32.8	4.3	238062	2	AC122579	AC122579 Rattus no
1363	32.8	4.3	239576	2	AC111231	AC111231 Rattus no
1364	32.8	4.3	241887	2	AC094044	AC094044 Rattus no
1365	32.8	4.3	243996	2	AC103098	AC103098 Rattus no
1366	32.8	4.3	244650	2	AC106532	AC106532 Rattus no
1367	32.8	4.3	244761	2	AC093963	AC093963 Rattus no
1368	32.8	4.3	244920	2	AC094336	AC094336 Rattus no
1369	32.8	4.3	248035	2	AC128391	AC128391 Rattus no
1370	32.8	4.3	250404	2	AC108966	AC108966 Rattus no
1371	32.8	4.3	251117	2	AC126815	AC126815 Rattus no
1372	32.8	4.3	251720	2	AC094479	AC094479 Rattus no
1373	32.8	4.3	252953	2	AC133431	AC133431 Rattus no
1374	32.8	4.3	254946	2	AC096598	AC096598 Rattus no
1375	32.8	4.3	255468	2	AC094339	AC094339 Rattus no
1376	32.8	4.3	257351	2	AC134160	AC134160 Rattus no
1377	32.8	4.3	260131	2	AC095733	AC095733 Rattus no
1378	32.8	4.3	261198	2	AC106528	AC106528 Rattus no
1379	32.8	4.3	267873	2	AC129399	AC129399 Rattus no
1380	32.8	4.3	271233	2	AC096597	AC096597 Rattus no
1381	32.8	4.3	281573	2	AC125743	AC125743 Rattus no
1382	32.8	4.3	282568	2	AC133660	AC133660 Rattus no
1383	32.8	4.3	300029	8	AE017090	AE017090 Oryza sat
1384	32.8	4.3	309145	2	AC105907	AC105907 Mus muscu
1385	32.8	4.3	312615	2	AC073722	AC073722 Mus muscu
1386	32.8	4.3	326606	2	AC110839	AC110839 Rattus no
1387	32.8	4.3	340000	9	HS21C080	AL163280 Homo sapi
1388	32.6	4.3	401	6	AX270287	AX270287 Sequence
1389	32.6	4.3	401	6	AX271818	AX271818 Sequence
1390	32.6	4.3	484	12	AY199369	AY199369 Arabidops
1391	32.6	4.3	537	11	G84037	G84037 S208P6826RG
1392	32.6	4.3	570	3	AF504492	AF504492 Andrena c
1393	32.6	4.3	603	11	BV012229	BV012229 MASC STS1
1394	32.6	4.3	1152	10	RATHFGFRG	LI9110 Rat c_lone
1395	32.6	4.3	1258	10	RATHFGFRF	LI9109 Rattus norv
1396	32.6	4.3	1302	9	AF090946	AF090946 Homo sapi
1397	32.6	4.3	1698	5	BX933064	BX933064 Gallus ga
1398	32.6	4.3	2000	6	AX509884	AX509884 Sequence
1399	32.6	4.3	2015	10	RRFIBGFC	Z35139 R.rattus mR
1400	32.6	4.3	2078	5	AY168630	AY168630 Eptatretu
1401	32.6	4.3	2117	10	RRFIBGFB	Z35138 R.rattus mR
1402	32.6	4.3	2595	6	AX684826	AX684826 Sequence
1403	32.6	4.3	2595	6	AX684828	AX684828 Sequence
1404	32.6	4.3	2623	9	AB063029	AB063029 Macaca fa
1405	32.6	4.3	2875	8	KLLACSA	X06215 Kluyveromyc
1406	32.6	4.3	2897	6	AX286948	AX286948 Sequence

1407	32.6	4.3	3721	8	YSKLAC9	M15210 Yeast (K.la
1408	32.6	4.3	4718	6	CQ588389	CQ588389 Sequence
1409	32.6	4.3	5072	4	AY173048	AY173048 Bos tauru
1410	32.6	4.3	5192	4	AY244709	AY244709 Bos tauru
1411	32.6	4.3	10352	1	AE006682	AE006682 Sulfolobu
1412	32.6	4.3	47565	9	AL512376	AL512376 Human DNA
1413	32.6	4.3	54417	9	AC108511	AC108511 Homo sapi
1414	32.6	4.3	56323	2	AC100972	AC100972 Mus muscu
1415	32.6	4.3	65957	2	AC014595	AC014595 Drosophil
1416	32.6	4.3	75839	2	AC037462	AC037462 Homo sapi
1417	32.6	4.3	80531	2	HSV460E1	AL008882 Homo sapi
1418	32.6	4.3	81493	8	AT81KGEN	X98130 Arabidopsis
1419	32.6	4.3	82646	8	AB028611	AB028611 Arabidops
1420	32.6	4.3	93045	8	ATT32M21	AL162875 Arabidops
1421	32.6	4.3	93426	9	AT1359732	AL359732 Human DNA
1422	32.6	4.3	94255	9	AC003090	AC003090 Homo sapi
1423	32.6	4.3	94884	8	AP004531	AP004531 Lotus cor
1424	32.6	4.3	101340	2	AC018104	AC018104 Drosophil
1425	32.6	4.3	108752	2	AC120825	AC120825 Homo sapi
1426	32.6	4.3	108886	2	AC145884	AC145884 Pan trogl
1427	32.6	4.3	110000	2	AC107252_3	Continuation (4 of
1428	32.6	4.3	110000	2	AC141403_0	AC141403 Homo sapi
1429	32.6	4.3	110000	8	CR380958_03	Continuation (4 of
1430	32.6	4.3	110000	8	CR382124_10	Continuation (11 o
1431	32.6	4.3	110000	9	AF491780_09	Continuation (10 o
1432	32.6	4.3	110324	2	AC136288	AC136288 Medicago
1433	32.6	4.3	110514	8	F7G19	AC000106 Sequence
1434	32.6	4.3	112922	9	AC020940	AC020940 Homo sapi
1435	32.6	4.3	112944	9	AC025761	AC025761 Homo sapi
1436	32.6	4.3	115351	8	CNS08C9B	AL732536 Oryza sat
1437	32.6	4.3	120375	8	AC126791	AC126791 Medicago
1438	32.6	4.3	125020	9	AF429315	AF429315 Homo sapi
1439	32.6	4.3	125377	2	AC118135	AC118135 Homo sapi
1440	32.6	4.3	128207	5	AC146503	AC146503 Danio rer
1441	32.6	4.3	128444	2	AF214634	AF214634 Homo sapi
1442	32.6	4.3	128821	9	AC108687	AC108687 Homo sapi
1443	32.6	4.3	129164	9	AC096547	AC096547 Homo sapi
1444	32.6	4.3	129196	8	AC134522	AC134522 Medicago
1445	32.6	4.3	130330	9	AC147137	AC147137 Pan trogl
1446	32.6	4.3	131184	9	HS2137	AL078474 Homo sapi
1447	32.6	4.3	133029	9	AL359094	AL359094 Human DNA
1448	32.6	4.3	137582	2	AC148726	AC148726 Pongo pyg
1449	32.6	4.3	137659	9	AL139232	AL139232 Human DNA
1450	32.6	4.3	141612	9	AC079093	AC079093 Homo sapi
1451	32.6	4.3	141883	8	OSJN00271	AL731626 Oryza sat
1452	32.6	4.3	143985	2	AC102716	AC102716 Mus muscu
1453	32.6	4.3	144319	9	AC007968	AC007968 Homo sapi
1454	32.6	4.3	145291	2	AC011799	AC011799 Homo sapi
1455	32.6	4.3	145629	2	AC099498	AC099498 Homo sapi
1456	32.6	4.3	145902	2	CR450826	CR450826 Danio rer
1457	32.6	4.3	146984	2	AC129814	AC129814 Rattus no
1458	32.6	4.3	147123	2	AC027030	AC027030 Homo sapi
1459	32.6	4.3	148362	10	AC138267	AC138267 Mus muscu
1460	32.6	4.3	148659	2	AC016108	AC016108 Homo sapi
1461	32.6	4.3	150662	2	AC114906	AC114906 Mus muscu
1462	32.6	4.3	150949	2	AC021600	AC021600 Homo sapi
1463	32.6	4.3	151133	2	BX950195	BX950195 Danio rer
1464	32.6	4.3	151834	9	AP004195	AP004195 Homo sapi
1465	32.6	4.3	152857	2	CR450744	CR450744 Danio rer
1466	32.6	4.3	152896	2	AC110665	AC110665 Canis fam
1467	32.6	4.3	153670	2	AL355295	AL355295 Homo sapi
1468	32.6	4.3	153764	9	AL355350	AL355350 Human DNA
1469	32.6	4.3	154726	9	AL445923	AL445923 Human DNA
1470	32.6	4.3	155731	9	AP001205	AP001205 Homo sapi
1471	32.6	4.3	156044	2	AC103897	AC103897 Papio anu
1472	32.6	4.3	157168	9	AL137018	AL137018 Human DNA
1473	32.6	4.3	157644	2	AL731770	AL731770 Homo sapi
1474	32.6	4.3	158610	10	AC122456	AC122456 Mus muscu
1475	32.6	4.3	158847	5	AL928619	AL928619 Zebrafish
1476	32.6	4.3	159226	9	AC142306	AC142306 Pan trogl
1477	32.6	4.3	159226	9	AC142306	AC142306 Pan trogl
1478	32.6	4.3	160436	9	AC146454	AC146454 Pan trogl
1479	32.6	4.3	160545	9	AC036214	AC036214 Homo sapi
1480	32.6	4.3	161310	9	AL445585	AL445585 Human DNA
1481	32.6	4.3	162165	2	AL162496	AL162496 Homo sapi
1482	32.6	4.3	164171	2	CR388067	CR388067 Danio rer
1483	32.6	4.3	164577	8	OSJN00169	AL662969 Oryza sat
1484	32.6	4.3	164839	9	AC147340	AC147340 Pan trogl
1485	32.6	4.3	164839	9	AC147340	AC147340 Pan trogl
1486	32.6	4.3	167108	9	CNS01RHA	AL161666 Human chr
1487	32.6	4.3	167472	5	BX001041	BX001041 Zebrafish
1488	32.6	4.3	168042	2	AC025931	AC025931 Homo sapi
1489	32.6	4.3	168159	9	AC147131	AC147131 Pan trogl
1490	32.6	4.3	169159	9	AL596179	AL596179 Human DNA
1491	32.6	4.3	169968	2	CR388128	CR388128 Danio rer
1492	32.6	4.3	170498	3	AC008094	AC008094 Drosophil
1493	32.6	4.3	171330	5	AL929040	AL929040 Zebrafish
1494	32.6	4.3	173691	9	AC022101	AC022101 Homo sapi
1495	32.6	4.3	173919	9	AC067837	AC067837 Homo sapi
1496	32.6	4.3	176805	2	AC107073	AC107073 Homo sapi
1497	32.6	4.3	178453	9	AC016144	AC016144 Homo sapi
1498	32.6	4.3	178560	2	AC134877	AC134877 Homo sapi
1499	32.6	4.3	178606	2	AC040906	AC040906 Homo sapi
1500	32.6	4.3	179117	2	AC113254	AC113254 Rattus no
ALIGNMENTS						
RESULT 1						
AR252552						
LOCUS	AR252552	766 bp	DNA	linear	PAT 20-DEC-2002	
DEFINITION	Sequence 257 from patent US 6478825.					
ACCESSION	AR252552					
VERSION	AR252552.1	GI:27300460				
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 766)					
AUTHORS	Winterbottom,J.M., Shimp,L., Boyce,T.M. and Kaes,D.					
TITLE	Implant, method of making same and use of the implant for the treatment of bone defects					
JOURNAL	Patent: US 6478825-A 257 12-NOV-2002;					
FEATURES	Location/Qualifiers					
source	1. .766					
ORIGIN	/organism="unknown"					
	/mol_type="genomic DNA"					
Query Match	100.0%;	Score 766;	DB 6;	Length 766;		
Best Local Similarity	100.0%;	Pred. No. 2.7e-208;				
Matches 766;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;		
QY	1	GGCTCGAGCGTTTCTGAGCCAGGGGTGACCATGACCTGCTGCGAAGGATGGACATCCTGC	60			
Db	1	GGCTCGAGCGTTTCTGAGCCAGGGGTGACCATGACCTGCTGCGAAGGATGGACATCCTGC	60			
QY	61	AATGGATTACGCTGCTGTTTCTACTGCTGTAGGAGTAGTTCTCAATGCGATACCTCTA	120			
Db	61	AATGGATTACGCTGCTGTTTCTACTGCTGTAGGAGTAGTTCTCAATGCGATACCTCTA	120			
QY	121	ATTGTCAGCTTAGTTGAGGAACCAATTTTCTCAAAACCCCATCTCTTGGTTTGAGTGG	180			
Db	121	ATTGTCAGCTTAGTTGAGGAACCAATTTTCTCAAAACCCCATCTCTTGGTTTGAGTGG	180			
QY	181	TGGTTCACGGAATTATAGGACGAGGTCTGATGGCCATTCCAGCAACAACATGTCCTTG	240			
Db	181	TGGTTCACGGAATTATAGGACGAGGTCTGATGGCCATTCCAGCAACAACATGTCCTTG	240			
QY	241	ACAGCAAGAAAAAGAGCGTGTGCAACAACAGAACTGGAATGTTTCTTTCATATTTTTC	300			
Db	241	ACAGCAAGAAAAAGAGCGTGTGCAACAACAGAACTGGAATGTTTCTTTCATATTTTTC	300			
QY	301	AGTGTGATCAGAGTCATTGGTGTCTGTATTGTCATGCTGATATCCATCCAGGCTCTCTTA	360			

Db 301 AGTGTGATCACAGTCATTGGTGGTCTGTATTGCGATGCTGATATCCATCCAGGCTCTCTTA 360
Qy 361 AAAGGTCTCTCATGTGTAAATCTCCAAGCAACAGTAATGCCAATTTGGAATTTTCATTG 420
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Qy 421 AAAAAATCAGTGACATTCATCAGAAATCCTTCAACTTGCAGTGGTTTTTCAATGACTCT 480
Db 421 AAAAAATCAGTGACATTCATCAGAAATCCTTCAACTTGCAGTGGTTTTTCAATGACTCT 480
Qy 481 TGTGCACCTCCTACTGTTTCAATAAAACCCACAGTAACGACACCATGGCGAGTGGCTGG 540
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Qy 541 AGAGCATCTAGTTCCACTTCGATTTCTGAAGAAAAACAAACATAGGCTTATCCACTTCTCA 600
Db 541 AGAGCATCTAGTTCCACTTCGATTTCTGAAGAAAAACAAACATAGGCTTATCCACTTCTCA 600
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Qy 661 GTATCGGTTTCTTGGCTGTCTGTGGAGTCTCTAAGCGAAGAAGTCAAATTTGTGTAG 720
Db 661 GTATCGGTTTCTTGGCTGTCTGTGGAGTCTCTAAGCGAAGAAGTCAAATTTGTGTAG 720
Qy 721 TTTAATGGGAATAAAATGTAAGTATCAGTAGTTTGAAAAA 766
Db 721 TTTAATGGGAATAAAATGTAAGTATCAGTAGTTTGAAAAA 766

RESULT 2
AX092316 LOCUS AX092316 766 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 47 from Patent WO0116318.
ACCESSION AX092316
VERSION AX092316.1 GI:13444472

KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Eaton,D.L., Filvaroff,E., Gerritsen,M.E., Goddard,A.,
Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Watanabe,C.K. and
Wood,W.I.

TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0116318-A 47 08-MAR-2001;
Genentech, Inc. (US)

FEATURES
source Location/Qualifiers
1..766
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 100.0%; Score 766; DB 6; Length 766;
Best Local Similarity 100.0%; Pred. No. 2.7e-208;
Matches 766; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCTCGAGCGTTTCTGAGCCAGGGGTGACCATGACCTGCTCGAAGGATGGACATCCTGC 60
Db 1 GGCTCGAGCGTTTCTGAGCCAGGGGTGACCATGACCTGCTCGAAGGATGGACATCCTGC 60

Qy 61 AATGGATTACGCTGCTGGTTCTACTGCTGTAGGAGTAGTTCTCAATGCGATACCTCTA 120
Db 61 AATGGATTACGCTGCTGGTTCTACTGCTGTAGGAGTAGTTCTCAATGCGATACCTCTA 120

Qy 121 ATTGTCAGCTTAGTTGAGGAAGACCAATTTCTCAAAACCCCATCTCTTGTCTTTGAGTGG 180
Db 121 ATTGTCAGCTTAGTTGAGGAAGACCAATTTCTCAAAACCCCATCTCTTGTCTTTGAGTGG 180

Qy 181 TGGTTCACAGGAATTATAGGAGCAGGTCGTGATGGCCATTCCAGCAACAACAAATGTCCTTG 240
Db 181 TGGTTCACAGGAATTATAGGAGCAGGTCGTGATGGCCATTCCAGCAACAACAAATGTCCTTG 240
Qy 241 ACAGCAAGAAAAAGAGCGTGTGCAACAACAGAACTGGAATGTTTCTTTCATCATTTTTC 300
Db 241 ACAGCAAGAAAAAGAGCGTGTGCAACAACAGAACTGGAATGTTTCTTTCATCATTTTTC 300
Qy 301 AGTGTGATCACAGTCATTGGTGTCTCTGTATTGTCATGCTGATATCCATCCAGGCTCTCTTA 360
Db 301 AGTGTGATCACAGTCATTGGTGTCTCTGTATTGTCATGCTGATATCCATCCAGGCTCTCTTA 360
Qy 361 AAAGGTCCTCTCATGTGTAATTTCTCCAAGCAACAGTAATGCCAATTTGTGAATTTTCATTG 420
Db 361 AAAGGTCCTCTCATGTGTAATTTCTCCAAGCAACAGTAATGCCAATTTGTGAATTTTCATTG 420
Qy 421 AAAAAATCAGTGACATTCATCCAGAAATCCTTCAACTTGCAGTGGTTTTTCAATGACTCT 480
Db 421 AAAAAATCAGTGACATTCATCCAGAAATCCTTCAACTTGCAGTGGTTTTTCAATGACTCT 480
Qy 481 TGTGCACCTCCTACTGTTTCAATAAAACCCACAGTAACGACACCATGGCGAGTGGCTGG 540
Db 481 TGTGCACCTCCTACTGTTTCAATAAAACCCACAGTAACGACACCATGGCGAGTGGCTGG 540
Qy 541 AGAGCATCTAGTTTCCACTTCGATTTCTGAAGAAAAACAAACATAGGCTTATCCACTTCTCA 600
Db 541 AGAGCATCTAGTTTCCACTTCGATTTCTGAAGAAAAACAAACATAGGCTTATCCACTTCTCA 600
Qy 601 GTATTTTGTAGTCTATTGCTTGTGGAATTTCTGGAGGTCCTGTTTGGGCTCAGTCAGATA 660
Db 601 GTATTTTGTAGTCTATTGCTTGTGGAATTTCTGGAGGTCCTGTTTGGGCTCAGTCAGATA 660
Qy 661 GTATCGGTTTCTTGGCTGTCTGTGGAGTCTCTAAGCGAAGAAGTCAAATTTGTGTAG 720
Db 661 GTATCGGTTTCTTGGCTGTCTGTGGAGTCTCTAAGCGAAGAAGTCAAATTTGTGTAG 720
Qy 721 TTTAATGGGAATAAAATGTAAGTATCAGTAGTTTGAAAAA 766
Db 721 TTTAATGGGAATAAAATGTAAGTATCAGTAGTTTGAAAAA 766

RESULT 3
AX376130 LOCUS AX376130 766 bp DNA linear PAT 01-MAR-2002
DEFINITION Sequence 197 from Patent WO0168848.
ACCESSION AX376130
VERSION AX376130.1 GI:19170457

KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Baker,K.P., Chen,J., Desnoyers,L., Goddard,A., Godowski,P.J.,
Gurney,A.L., Pan,J., Smith,V., Watanabe,C.K., Wood,W.I. and
Zhang,Z.

TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0168848-A 197 20-SEP-2001;
Genentech, Inc. (US)

FEATURES
source Location/Qualifiers
1..766
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 100.0%; Score 766; DB 6; Length 766;
Best Local Similarity 100.0%; Pred. No. 2.7e-208;
Matches 766; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCTCGAGCGTTTCTGAGCCAGGGGTGACCATGACCTGCTCGAAGGATGGACATCCTGC 60
Db 1 GGCTCGAGCGTTTCTGAGCCAGGGGTGACCATGACCTGCTCGAAGGATGGACATCCTGC 60

Db	1	GGCTCGAGCGTTTCTGAGCCAGGGGTGACCATGACCTGCTGCGAAGGATGGACATCCTGC	60	source	1. .766	
QY	61	AATGGATTGAGCGTCTGGTTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATACCTCTA	120		/organism="Homo sapiens"	
Db	61				/mol_type="unassigned DNA"	
QY	121	ATTGTCAGCTTAGTTGAGGAAGACCAATTTTCTCAAAACCCCACTCTCTTGCTTTGAGTGG	180		/db_xref="taxon:9606"	
Db	121	ATTGTCAGCTTAGTTGAGGAAGACCAATTTTCTCAAAACCCCACTCTCTTGCTTTGAGTGG	180	ORIGIN		
QY	181	TGGTCCCAGGAATTATAGGAGCAGGTCTGATGGCCATTCAGCAACAACAATGTCCTTG	240	Query Match	100.0%;	Score 766; DB 6; Length 766;
Db	181	TGGTCCCAGGAATTATAGGAGCAGGTCTGATGGCCATTCAGCAACAACAATGTCCTTG	240	Best Local Similarity	100.0%;	Pred. No. 2.7e-208;
QY	241	ACAGCAAGAAAAAGAGCGTCTGCAACAACAGAACTGGAATGTTTTCATCATATTTTC	300	Matches	766; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Db	241	ACAGCAAGAAAAAGAGCGTCTGCAACAACAGAACTGGAATGTTTTCATCATATTTTC	300			
QY	301	AGTGTGATCACAGTCATTTGGTCTGTGATTCGATGATCCATCCAGGCTCTCTTA	360			
Db	301	AGTGTGATCACAGTCATTTGGTCTGTGATTCGATGATCCATCCAGGCTCTCTTA	360			
QY	361	AAAGTCTCTCATGTGTAATTTCTCAAGCAACAGTAATGCCAATTTGTAATTTTCATTG	420			
Db	361	AAAGTCTCTCATGTGTAATTTCTCAAGCAACAGTAATGCCAATTTGTAATTTTCATTG	420			
QY	421	AAAAACATCAGTGACATTCATCCAGAATCCTTCAACTTGCAGTGGTTTTTCATGACTCT	480			
Db	421	AAAAACATCAGTGACATTCATCCAGAATCCTTCAACTTGCAGTGGTTTTTCATGACTCT	480			
QY	481	TGTGCACCTCCTACTGGTTTCAATAAAACCCACCAGTAACGACACCATGGCGAGTGGTGG	540			
Db	481	TGTGCACCTCCTACTGGTTTCAATAAAACCCACCAGTAACGACACCATGGCGAGTGGTGG	540			
QY	541	AGAGCATCTAGTTTCCACTTCGATTCTGAAGAAAAACAACATAGGCTTATCCACTTCTCA	600			
Db	541	AGAGCATCTAGTTTCCACTTCGATTCTGAAGAAAAACAACATAGGCTTATCCACTTCTCA	600			
QY	601	GTATTTTTAGTCTATTTGCTTGTGGAATTTCTGAGGTCCTGTTGGGCTCAGTCAGATA	660			
Db	601	GTATTTTTAGTCTATTTGCTTGTGGAATTTCTGAGGTCCTGTTGGGCTCAGTCAGATA	660			
QY	661	GTATCGGTTTCCCTGGCTGTCTGTGGAGTCTCTAAGCGAAGAGTCAAAATTGTGTAG	720			
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QY	721	TTTAATGGGAATAAAATGTAAGTATCAGTAGTTTGAAAAAATAAAAA	766			
Db	721	TTTAATGGGAATAAAATGTAAGTATCAGTAGTTTGAAAAAATAAAAA	766			
RESULT 4						
AX403370						
LOCUS	AX403370	766 bp	DNA	linear	PAT 14-JUN-2002	
DEFINITION	Sequence 257 from Patent WO0073454.					
ACCESSION	AX403370					
VERSION	AX403370.1	GI:21436906				
KEYWORDS						
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
AUTHORS	1					
	Ashkenazi, A.J., Baker, K.P., Botstein, D., Desnovers, L., Eaton, D., Ferrara, N., Gerber, H., Gerritsen, M., Goddard, A., Godowski, P., Grimaldi, C.J., Gurney, A.L., Kljavin, I., Napier, M.A., Pan, J., Paoni, N.F., Roy, M., Stewart, T.A., Tumas, D., Watanabe, C.K., Williams, P., Wood, W.I. and Zhang, Z.					
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding the same					
JOURNAL	Patent: WO 0073454-A 257 07-DEC-2000; Genentech Inc. (US)					
FEATURES	Location/Qualifiers					

RESULT 5
AY358671
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AY358671
Homo sapiens clone DNA5855 TCCE518 (UNQ518) mRNA, complete cds.
AY358671
AY358671.1 GI:37182463
FLI_CDNA.
Homo sapiens (human)
Homo sapiens

766 bp mRNA linear PRI 03-OCT-2003

REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
gene
CDS
ORIGIN
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
Matches 766; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 GGCTCGAGCGTTTCTGAGCCAGGGGTGACCATGACCTGCTGCGAAGGATGGACATCCTGC 60
1 GGCTCGAGCGTTTCTGAGCCAGGGGTGACCATGACCTGCTGCGAAGGATGGACATCCTGC 60
61 AATGATTTCAGCCTGCTGGTTCTACTGCTGTAGGAGTAGTTCTCAATGGCATACCTCTA 120
61 AATGATTTCAGCCTGCTGGTTCTACTGCTGTAGGAGTAGTTCTCAATGGCATACCTCTA 120
121 ATTGTCAGCTTAGTTGAGGAAGACCAATTTCTCAAAACCCCATCTCTTGTGTTGAGTGG 180
121 ATTGTCAGCTTAGTTGAGGAAGACCAATTTCTCAAAACCCCATCTCTTGTGTTGAGTGG 180
181 TGGTTCCTCCAGGAATTATAGGAGCAGGCTGTGATGGCCATTCAGCAACAACAATGTCCTTG 240
181 TGGTTCCTCCAGGAATTATAGGAGCAGGCTGTGATGGCCATTCAGCAACAACAATGTCCTTG 240
241 ACAGCAAGAAAAAGAGCGGTGCTGCAACAACAGAACTGGAATGTTCTTTTCATCATTTTC 300
241 ACAGCAAGAAAAAGAGCGGTGCTGCAACAACAGAACTGGAATGTTCTTTTCATCATTTTC 300
301 AGTGTGATCACAGTCATTGGTGTCTGTATTGTCATGCTGATATCCATCCAGGCTCTCTTA 360
301 AGTGTGATCACAGTCATTGGTGTCTGTATTGTCATGCTGATATCCATCCAGGCTCTCTTA 360
361 AAAGTCTCTCATGTGTAATTTCTCAAGCAACAGTAATGCCAATTTGTGAATTTTCATTG 420

Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 766)
Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,
Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,
Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,
Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C.,
Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V.,
Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,D., Woods,K.,
Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
Goddard,A., Wood,W.I. and Godowski,P.
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
Effort to Identify Novel Human Secreted and Transmembrane Proteins:
A Bioinformatics Assessment
Genome Res. 13 (10), 2265-2270 (2003)
12975309
2 (bases 1 to 766)
Clark,H.F.
Direct Submission
Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
Inc., 1 DNA Way, South San Francisco, CA 94080, USA
Location/Qualifiers
1. .766
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Db 361 AAAGTCTCTCATGTGTAATTTCTCAAGCAACAGTAATGCCAATTTGTGAATTTTCATTG 420
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QY 481 TGTGCACCTCCTACTGTTTCAATAAAACCCACAGTAACGACACCATGGCGAGTGGCTGG 540
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Db 661 GTCATCGGTTTCTTGGCTGTCTGTGGAGTCTCTAAGCGAAGAACATTAATTTGTGTAG 720
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RESULT 6
AK026453
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DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source
CDS
AK026453
Homo sapiens cDNA: FLJ22800 fis, clone KAI2630.
AK026453
AK026453.1 GI:10439322
oligo capping; fis (full insert sequence).
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1
Kawakami,T., Noguchi,S., Itoh,T., Shigeta,K., Senba,T.,
Matsumura,K., Nakajima,Y., Mizuno,T., Morinaga,M., Tanigami,A.,
Fujiwara,T., Ono,T., Yamada,K., Fujii,Y., Ozaki,K., Hirao,M.,
Ohmori,Y., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T., Shibahara,T.,
Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.
NEDO human cDNA sequencing project
Unpublished
2 (bases 1 to 2308)
Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Isogai,T.,
Shibahara,T., Tanaka,T. and Nakamura,Y.
Direct Submission
Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science,
University of Tokyo, Laboratory of Genome Structure Analysis, Human
Genome Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639,
Japan (E-mail:flcdna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
Fax:81-3-5449-5416)
NEDO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan; cDNA full insert
sequencing: Research Association for Biotechnology; cDNA library
construction, 5'- & 3'-end one pass sequencing: Departent of
Virology and Human Genome Center, Institute of Medical Science,
University of Tokyo (partly supported by Science and Technology
Agency).
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ORIGIN													
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QY	7	AGCGTTTCTGAGCCAGGGGTGACCATGACCTGCTGCGAAGGATGACATCCTGCAATGGA	66										
Db	14	AACGTTTCTGAGCCAGGGGTGACCATGACCTGCTGCGAAGGATGACATCCTGCAATGGA	73										
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QY	187	CCAGGAATTATAGAGCAGGTCGTGATGGCCATTCCAGCAACAACAATGTCCTTGACAGCA	246										
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QY	307	ATCACAGTCATTGGTGCTCTGTATTGCATGCTGATATCCATCCAGGCTCTCTTTAAAGGT	366										
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QY	607	TTAGGTCTATTGCTTGTGGAAATCTGGAGGTCCTGTTTGGGCTCAGTCAGATAGTCATC	666										
Db	614	TTAGGTCTATTGCTTGTGGAAATCTGGAGGTCCTGTTTGGGCTCAGTCAGATAGTCATC	673										
QY	667	GGTTTCCTTGGCTGCTGTGTGGAGTCTCTAAGCGAAGAAGTCAAATTTGTGAGTTAAT	726										
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QY	727	GGGAATAAAATGTAAGTATCAGTAGTTTGAATAAA 761											
Db	734	GGGAATAAAATGTAAGTATCAGTAGTTTGAATAAA 768											
RESULT 7													
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LOCUS		AC079784											
DEFINITION		Homo sapiens clone RP11-395L7, LOW-PASS SEQUENCE SAMPLING.											
ACCESSION		AC079784											
VERSION		AC079784.1		GI:10048030									

KEYWORDS	HTG; HTGS_PHASE0.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 46778)
TITLE	Waterston,R.H.
JOURNAL	The sequence of Homo sapiens clone
REFERENCE	Unpublished
AUTHORS	2 (bases 1 to 46778)
TITLE	Waterston,R.H.
JOURNAL	Direct Submission
COMMENT	Submitted (10-SEP-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA Center project name: H NH0395L07. * NOTE: This record contains 85 individual * sequencing reads that have not been assembled into * contigs. Runs of N are used to separate the reads * and the order in which they appear is completely * arbitrary. Low-pass sequence sampling is useful for * identifying clones that may be gene-rich and allows * overlap relationships among clones to be deduced. * However, it should not be assumed that this clone * will be sequenced to completion. In the event that * the record is updated, the accession number will * be preserved. * 1 881: contig of 881 bp in length * 882 891: gap of unknown length * 892 1193: contig of 302 bp in length * 1194 1203: gap of unknown length * 1204 1745: contig of 542 bp in length * 1746 1755: gap of unknown length * 1756 2630: contig of 875 bp in length * 2631 2640: gap of unknown length * 2641 3507: contig of 867 bp in length * 3508 3517: gap of unknown length * 3518 4441: contig of 924 bp in length * 4442 4451: gap of unknown length * 4452 4972: contig of 521 bp in length * 4973 4982: gap of unknown length * 4983 5891: contig of 909 bp in length * 5892 5901: gap of unknown length * 5902 6445: contig of 544 bp in length * 6446 6455: gap of unknown length * 6456 6943: contig of 488 bp in length * 6944 6953: gap of unknown length * 6954 7494: contig of 541 bp in length * 7495 7504: gap of unknown length * 7505 7970: contig of 466 bp in length * 7971 7980: gap of unknown length * 7981 8845: contig of 865 bp in length * 8846 8855: gap of unknown length * 8856 9297: contig of 442 bp in length * 9298 9307: gap of unknown length * 9308 10207: contig of 900 bp in length * 10208 10217: gap of unknown length * 10218 10625: contig of 408 bp in length * 10626 10635: gap of unknown length * 10636 11468: contig of 833 bp in length * 11469 11478: gap of unknown length * 11479 11996: contig of 518 bp in length * 11997 12006: gap of unknown length * 12007 12502: contig of 496 bp in length * 12503 12512: gap of unknown length * 12513 12968: contig of 456 bp in length * 12969 12978: gap of unknown length * 12979 13496: contig of 518 bp in length * 13497 13506: gap of unknown length * 13507 14048: contig of 542 bp in length * 14049 14058: gap of unknown length * 14059 14426: contig of 368 bp in length * 14427 14436: gap of unknown length

* 14437 14940: contig of 504 bp in length
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* 15955 16410: contig of 456 bp in length
* 16411 16420: gap of unknown length
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* 16869 16878: gap of unknown length
* 16879 17428: contig of 550 bp in length
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* 17439 17946: contig of 508 bp in length
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* 45739 46248: contig of 510 bp in length
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* 46259 46778: contig of 520 bp in length.

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Best Local Similarity 95.8%; Pred. No. 6.9e-84;
Matches 341; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 406 TGTGAATTTTCATTGAAAAACATCAGTGACATTCATCCAGAAATCCTTCAACTTGCAGTGG 465
Db 28408 TCTGATTTTATCTTTTGTTCAGTGACATTCATCCAGAAATCCTTCAACTTGCAGTGG 28349

QY 466 TTTTTCATGACTCTGTGCACCTCCTACTGTTTCAATAAACCCACCAGTAACGACACC 525
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Db 28288 ATGCGGAGTGGCTGGAGAGCATCTAGTTTCCACATTCGATTCTGAAGAAAAACAACATAGG 28229

QY 586 CTTATCCACTTCTCAGTATTTTAGGTCTATTTGCTGTTTGAATTTCTGGAGGTCCTGTTT 645
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QY 646 GGGCTCAGTCAGATAGTCATCGGTTTCCCTTGGTCTGTGTGGAGTCTTAAGCGAAGA 705

Db 28168 GGGCTCAGTCAGATAGTCATCGGTTTCCTTGGCTGTCTGTGTGGAGTCTCTAAGCGAAGA 28109

QY 706 AGTCAAAATTGTGTAGTTTAATGGGAATAAAATGTAAGTATCATGAGTATTTGAAAAAA 761
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Db 28108 AGTCAAAATTGTGTAGTTTAATGGGAATAAAATGTAAGTATCATGAGTATTTGAATTAA 28053

RESULT 8

AC097662/c

LOCUS AC097662 206624 bp DNA linear PRI 14-JUL-2002

DEFINITION Homo sapiens BAC clone RP11-563C6 from 2, complete sequence.

ACCESSION AC097662

VERSION AC097662.5 GI:21617782

KEYWORDS HTG.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 206624)

Sulston,J.E. and Waterston,R.

Toward a complete human genome sequence

Genome Res. 8 (11), 1097-1108 (1998)

99063792

9847074

2 (bases 1 to 206624)

Harris,A., Meyer,R. and Nguyen,C.

The sequence of Homo sapiens BAC clone RP11-563C6

Unpublished (2001)

3 (bases 1 to 206624)

Waterston,R.H.

Direct Submission

Submitted (20-OCT-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

4 (bases 1 to 206624)

Waterston,R.H.

Direct Submission

Submitted (29-MAR-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

5 (bases 1 to 206624)

Waterston,R.H.

Direct Submission

Submitted (27-JUN-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

6 (bases 1 to 206624)

Waterston,R.

Direct Submission

Submitted (14-JUL-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

On Jun 27, 2002 this sequence version replaced gi:19807939.

----- Genome Center

Center: Washington University Genome Sequencing Center

Center code: WUGSC

Web site: <http://genome.wustl.edu/gsc>

Contact: sapiens@watson.wustl.edu

----- Summary Statistics

Center project name: H_NH0563C06

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa,K., Woon,P.Y., Zhao,B., Frengen,E., Tateno,M., Catanese,J.J. and de Jong,P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>

VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-249A8, 2000 bp overlap; the clone sequenced to the right is RP11-107L21. Actual start of this clone is at base position 1 of RP11-563C6; actual end is at base position 206624 of RP11-563C6.

An unsure base exists at position 97277. A single plasmid subclone region exists between bases 127997 to 128158. Polymorphisms have been identified between AC107069 and AC097662. Data from AC107069 and AC105286 were used to finish this clone, AC097662.

FEATURES

Source

Location/Qualifiers

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repeat_region

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Query Match 43.3%; Score 332; DB 9; Length 206624;
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QY 406 TGTGAATTTTCATTGAAACATCAGTGACATTCATCCAGAATCCITCAACTTGCAGTG 465
Db 93128 TCTGATTTTATCTTTTGTTCAGTGACATTCATCCAGAATCCITCAACTTGCAGTG 93069
QY 466 TTTTCAATGACTCTTGTGCACCTCCTACTGGTTTCAATAAACCACCAGTAACGACACC 525

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Db 92948 CTTATCCACTTCTCAGTATTTTATAGTCTATTGCTTGTGGAATTTCTGGAGGTCCTGTTT 92889
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LOCUS AX246020 351 bp DNA linear PAT 28-SEP-2001
DEFINITION Sequence 950 from Patent WO0166753.
ACCESSION AX246020
VERSION AX246020.1 GI:15860694
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Williams,L.T., Escobedo,J., Innis,M.A., Garcia,P.D.,
Sudduth-Klinger,J., Reinhard,C., Randazzo,F., Kennedy,G.C., Pot,D.,
Kassam,A., Lamson,G., Drmanac,R., Crkvenjakov,R., Dickson,M.,
Drmanac,S., Labat,I., Leshkowitz,D., Kita,D., Garcia,V. and
Stache-Crain,B.
TITLE Human genes and gene expression products
JOURNAL Patent: WO 0166753-A 950 13-SEP-2001;
Chiron Corporation (US) ; Hyseq Inc. (US)
FEATURES
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Best Local Similarity 91.0%; Pred. No. 1.9e-64;
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QY 67 TTCAGCCTGCTGGTTCTACTGCTGTAGGAGTAGTTCTCAATGCGATACCT-CTAATTGT 125
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QY 126 CAGCTTAGTT-GAGGAAGACCAATTTTCTCAAAACCCCATCTCTTGTGTTGAGTGGT 184
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QY 185 TCCAGGAATTATAGGAGCAGGTCTGATGGCCATTCCAGCAACAACAATGTCCTTGACAG 244
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Phunkhang,P., Pierre,N., Rachupka,A., Ramasamy,U., Raymond,C.,
Retta,R., Rise,C., Rogov,P., Roman,J., Schauer,S., Schupback,R.,
Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N.,
Stojanovic,N., Stubbs,M., Talamas,J., Tesfaye,S., Theodore,J.,
Topham,K., Travers,M., Vassiliev,H., Venkataraman,V.S., Viel,R.,
Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L.,
Zimmer,A. and Zody,M.

Direct Submission

Submitted (19-MAY-2004) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

4 (bases 1 to 203478)

REFERENCE

AUTHORS

Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
Anderson,M., Anderson,S., Arachchi,H.M., Barna,N., Bastien,V.,
Bloom,T., Boguslavkiy,L., Boukhgalter,B., Camarata,J., Chang,J.,
Choepel,Y., Collymore,A., Cook,A., Cooke,P., Corum,B.,
DeArelano,K., Diaz,J.S., Dodge,S., Dooley,K., Dorris,L.,
Erickson,J., Faro,S., Ferreira,P., FitzGerald,M., Gage,D.,
Galgan,J., Gardyna,S., Graham,L., Grand-Pierre,N., Hafez,N.,
Hagopian,D., Hagos,B., Hall,J., Horton,L., Hulme,W., Iliev,I.,
Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Landers,T.,
Levine,R., Lindblad-Toh,K., Liu,G., Liu,X., Lui,A., Mabbitt,R.,
Maclean,C., Macdonald,P., Major,J., Manning,J., Matthews,C.,
McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,
Murphy,T., Naylor,J., Nguyen,C., Nguyen,T., Nicol,R., Norbu,C.,
O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K.,
Phunkhang,P., Pierre,N., Rachupka,A., Ramasamy,U., Raymond,C.,
Retta,R., Rise,C., Rogov,P., Roman,J., Schauer,S., Schupback,R.,
Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N.,
Stojanovic,N., Stubbs,M., Talamas,J., Tesfaye,S., Theodore,J.,
Topham,K., Travers,M., Vassiliev,H., Venkataraman,V.S., Viel,R.,
Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L.,
Zimmer,A. and Zody,M.

Direct Submission

Submitted (14-JUL-2004) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

On Jul 14, 2004 this sequence version replaced gi:47498220.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@broad.mit.edu

----- Project Information

Center project name: L28766

Center clone name: 404_A_6

FEATURES

source

Location/Qualifiers

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QY 489 TCCTACTGGTTTCAATAAACCCACAGTAACGACACCATGGCGAGTGGCTGGAGAGCATC 548
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QY 549 TAGTTTCCACTTCGATTCTGAAGAAAAACAACATAGGCTTATCCACTTCTCAGTATTTT 608
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Db 112727 GAGTCTCCTGCTTGTGGAATCCTGGAGCTCCTGTTGGGCTCAGTCAGATACATCTGG 112668

QY 669 TTTCTTGGCTGTCTGTGGAGTCTCTAAGCGAAGAGTCAAAATTGTGTAGTTTAATGG 728
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            ***, 2 unordered pieces.
ACCESSION  AC106407
VERSION    AC106407.5 GI:30581196
KEYWORDS   HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
SOURCE     Rattus norvegicus (Norway rat)
ORGANISM   Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE  1 (bases 1 to 209326)
AUTHORS   Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J.,
            Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
            Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
            Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
            Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
            Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
            Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
            Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
            Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
            Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
            Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
            Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
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            Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
            Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
            Gebrgeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
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            Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J.,
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            Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A.,
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            Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,
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Maheeshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A.,
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Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C.,
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Puzo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R.,
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Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J.,
Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H.,
Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D.,
Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J.,
Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C.,
Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K.,
Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J.,
Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F.,
Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K.,
Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,
Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
Weinstock,G. and Gibbs,R.A.
Direct Submission
Unpublished
2 (bases 1 to 209326)
Worley,K.C.
Direct Submission
Submitted (12-JAN-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 209326)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (13-MAY-2003) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On May 13, 2003 this sequence version replaced gi:24942449.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GKVI
Center clone name: CH230-133G12
----- Summary Statistics
Assembly program: Atlas 3.0;
Consensus quality: 204322 bases at least Q40
Consensus quality: 205593 bases at least Q30
Consensus quality: 206229 bases at least Q20
Estimated insert size: 213275; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
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* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
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Run on: January 24, 2005, 19:10:32 ; Search time 334 Seconds
(without alignments)
12039.091 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 4134886 seqs, 2624710521 residues
Total number of hits satisfying chosen parameters: 8269772
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

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2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
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10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ID	AAZ65043	standard; cDNA; 766 BP.				
DE	Membrane-bound protein PRO994 encoding cDNA.					
PN	WO9963088-A2.					
PD	09-DEC-1999.					
PA	(GETH) GENENTECH INC.					
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Best Local Similarity	100.0%;	Pred. No. 5.8e-222;				
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PN	WO200168848-A2.					
PD	20-SEP-2001.					
PA	(GETH) GENENTECH INC.					
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Best Local Similarity	100.0%;	Pred. No. 5.8e-222;				
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PN	WO200116318-A2.					
PD	08-MAR-2001.					
PA	(GETH) GENENTECH INC.					
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Best Local Similarity	100.0%;	Pred. No. 5.8e-222;				
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DE	Human PRO994 (UNQ518) nucleotide sequence SEQ ID NO:257.					
PN	WO200073454-A1.					
PD	07-DEC-2000.					
PA	(GETH) GENENTECH INC.					
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Best Local Similarity	100.0%;	Pred. No. 5.8e-222;				
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ID	ABS74401	standard; cDNA; 766 BP.				
DE	Human cDNA encoding secreted/transmembrane protein PRO994.					
PN	US2002119130-A1.					
PD	29-AUG-2002.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 766;	DB 6;	Length 766;		

Best Local Similarity 100.0%; Pred. No. 5.8e-222;

RESULT 6

ID ACA89473 standard; cDNA; 766 BP.

DE cDNA encoding human PRO polypeptide #99.

PN US2003036141-A1.

PD 20-FEB-2003.

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RESULT 7

ID ACA73483 standard; cDNA; 766 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #99.

PN US2003036146-A1.

PD 20-FEB-2003.

PA (GETH) GENENTECH INC.

Query Match

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RESULT 8

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DE Human secreted/transmembrane protein (PRO) cDNA #99.

PN US2003036162-A1.

PD 20-FEB-2003.

PA (GETH) GENENTECH INC.

Query Match

Best Local Similarity 100.0%; Score 766; DB 8; Length 766;

RESULT 9

ID ACA66632 standard; cDNA; 766 BP.

DE cDNA encoding human PRO protein #99.

PN US2003036137-A1.

PD 20-FEB-2003.

PA (GETH) GENENTECH INC.

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RESULT 10

ID ACA64335 standard; cDNA; 766 BP.

DE Novel human secreted and transmembrane protein PRO994 cDNA.

PN US2003003531-A1.

PD 02-JAN-2003.

PA (GETH) GENENTECH INC.

Query Match

Best Local Similarity 100.0%; Score 766; DB 8; Length 766;

RESULT 11

ID ACA91187 standard; cDNA; 766 BP.

DE Novel human secreted and transmembrane protein PRO994 cDNA.

PN US2003018173-A1.

PD 23-JAN-2003.

PA (GETH) GENENTECH INC.

Query Match

Best Local Similarity 100.0%; Score 766; DB 8; Length 766;

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ID ACD81564 standard; cDNA; 766 BP.

DE Human cDNA encoding secreted/transmembrane protein PRO994.

PN US2003009013-A1.

PD 09-JAN-2003.

PA (GETH) GENENTECH INC.

Query Match

Best Local Similarity 100.0%; Score 766; DB 8; Length 766;

RESULT 13

ID ACF20207 standard; cDNA; 766 BP.

DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.

PN US2003040063-A1.

PD 27-FEB-2003.

Query Match

Best Local Similarity 100.0%; Score 766; DB 8; Length 766;

RESULT 14

ID ACF19593 standard; cDNA; 766 BP.

DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.

PN US2003040064-A1.

PD 27-FEB-2003.

Query Match

Best Local Similarity 100.0%; Score 766; DB 8; Length 766;

RESULT 15

ID ACD21881 standard; cDNA; 766 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #99.

PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 16
ID ACF13046 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 17
ID ACD25149 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 18
ID ACF00198 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 19
ID ACA60386 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 20
ID ACA72255 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 21
ID ACD04779 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 22
ID ACD18240 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 23
ID ACD08247 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 24
ID ACA8681 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 25
ID ACA70123 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003036134-A1.

PD 20-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 26
ID ACD12345 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 27
ID ACC74260 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 28
ID ACD15888 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 29
ID ACD25456 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 30
ID ACD17933 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 31
ID ACC88220 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 32
ID ACD21574 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 33
ID ACD18641 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 34
ID ACA58833 standard; cDNA; 766 BP.
DE cDNA encoding human secreted polypeptide PRO994.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 35
ID ABX98251 standard; cDNA; 766 BP.
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 197.
PN US2003036156-A1.
PD 20-FEB-2003.

Query Match
Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
RESULT 36
ID ACD14002 standard; cDNA; 766 BP.
DE Human secreted polynucleotide #99.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
RESULT 37
ID ACD09782 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
RESULT 38
ID ACC88527 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
RESULT 39
ID ACD21267 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
RESULT 40
ID ABX75639 standard; cDNA; 766 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO994.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
RESULT 41
ID ACA64009 standard; cDNA; 766 BP.
DE cDNA encoding human PRO polypeptide #24.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
RESULT 42
ID ABX97842 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #99.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
RESULT 43
ID ACA97318 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
RESULT 44
ID ACA57781 standard; cDNA; 766 BP.
DE Human PRO994 cDNA.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
RESULT 45
ID ACD14309 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #99.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 8; Length 766;

Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 46
ID ACC91092 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
RESULT 47
ID ACC8834 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
RESULT 48
ID ACD07031 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #99.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
RESULT 49
ID ACA67482 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #99.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
RESULT 50
ID ACC81537 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
RESULT 51
ID ACA91273 standard; cDNA; 766 BP.
DE cDNA encoding human PRO polypeptide #24.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
RESULT 52
ID ACC89141 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
RESULT 53
ID ACC86497 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
RESULT 54
ID ACC89755 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
RESULT 55
ID ACC92934 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
RESULT 56
ID ACD45172 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein cdNA, #103.
PN US2003027162-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
RESULT 57
ID ACA72562 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #99.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
RESULT 58
ID ACA89080 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cdNA #99.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
RESULT 59
ID ACA69816 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cdNA #99.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
RESULT 60
ID ACA96959 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cdNA.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
RESULT 61
ID ACA90955 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cdNA.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
RESULT 62
ID ACA70737 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cdNA #99.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
RESULT 63
ID ACA95247 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cdNA.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
RESULT 64
ID ACD44303 standard; cDNA; 766 BP.
DE cDNA encoding human PRO994 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
RESULT 65
ID ACC86190 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cdNA, SEQ ID NO:197.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 8; Length 766;

Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 66
ID ACD45172 standard; cDNA; 766 BP.
DE Human secreted/transmembrane polypeptide PRO994 cdNA.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
RESULT 67
ID ACC90062 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cdNA, SEQ ID NO:197.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
RESULT 68
ID ACD12670 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cdNA #99.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
RESULT 69
ID ACF19900 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cdNA, SEQ ID NO:197.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
RESULT 70
ID ABX76844 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #99.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
RESULT 71
ID ACA73176 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cdNA.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
RESULT 72
ID ACA68719 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cdNA.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
RESULT 73
ID ACA74563 standard; cDNA; 766 BP.
DE cDNA encoding human PRO polypeptide #99.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
RESULT 74
ID ACA70430 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cdNA #99.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
RESULT 75
ID ACD14616 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #99.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 8; Length 766;
RESULT 76
ID ACD14616 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #99.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 8; Length 766;

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ID ACA93720 standard; cDNA; 766 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO994.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 77
ID ACA68288 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 78
ID ABX98753 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 79
ID ACA67294 standard; cDNA; 766 BP.
DE cDNA encoding human secreted polypeptide PRO994.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 80
ID ACC81230 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 81
ID ACA95554 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 82
ID ACD04472 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 83
ID ACC87913 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 84
ID ACF12575 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 85
ID ACH66267 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 86
ID ABX79474 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein cDNA, #103.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 87
ID ACA96290 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #99.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 88
ID ACA65064 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #99.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 89
ID ACA73790 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 90
ID ACA74202 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 91
ID ACA96597 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #99.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 92
ID ACD10703 standard; cDNA; 766 BP.
DE cDNA encoding human PRO polypeptide #99.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 93
ID ACC91399 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 94
ID ACA93495 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003022187-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 95
ID ACD02734 standard; cDNA; 766 BP.
DE cDNA encoding human PRO polypeptide #99.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 96
ID ACC87299 standard; cDNA; 766 BP.
```


DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 97
ID ACC85883 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 98
ID ABX81177 standard; DNA; 766 BP.
DE Novel human secreted or transmembrane protein PRO812 DNA.
PN US2003027985-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 99
ID ACA65371 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #99.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 100
ID ACA94188 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 101
ID ACA97932 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #99.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 102
ID ACA91434 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 103
ID ACA90648 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 104
ID ACD16195 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 105
ID ACD17356 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 106
ID ACC92013 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003040069-A1.

PD 27-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 107
ID ACD02321 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 108
ID ACA74870 standard; cDNA; 766 BP.
DE cDNA encoding human PRO polypeptide #99.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 109
ID ACA91741 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #99.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 110
ID ACA89312 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 111
ID ACA71385 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 112
ID ACC90785 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 113
ID ACA65795 standard; cDNA; 766 BP.
DE cDNA encoding human PRO protein #99.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 114
ID ACA68949 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 115
ID ACA92993 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003017476-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 116
ID ACA94940 standard; cDNA; 766 BP.
DE cDNA encoding human PRO polypeptide #99.
PN US2003017541-A1.

PD 23-JAN-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 117
ID ACD16502 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 118
ID ACD15581 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 119
ID ACA98471 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #24.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 120
ID ABX17077 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #73.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 121
ID ABX16684 standard; cDNA; 766 BP.
DE Human cDNA encoding secreted/transmembrane protein #99.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 8; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 122
ID ACA67932 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 123
ID ACA63396 standard; cDNA; 766 BP.
DE cDNA encoding human PRO polypeptide #24.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 124
ID ACA97625 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #99.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 125
ID ACA99074 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 126
ID ACC91706 standard; cDNA; 766 BP.

DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 127
ID ACD11117 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 128
ID ACD14967 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003044922-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 129
ID ACA88381 standard; cDNA; 766 BP.
DE Human secreted and transmembrane polypeptide PRO994 cDNA.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 130
ID ACD81888 standard; cDNA; 766 BP.
DE cDNA encoding human PRO994 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 131
ID ACD11731 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003032118-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 132
ID ACC95860 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003036135-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 133
ID ACF16423 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 134
ID ACF02541 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 135
ID ACF02848 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;

Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 136
ID ACF21435 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 137
ID ACF10119 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 138
ID ACF78012 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 139
ID ACD46717 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 140
ID ACD49480 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 141
ID ACF28247 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 142
ID ACD88937 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 143
ID ACD84332 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #99.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 144
ID ACD99106 standard; cDNA; 766 BP.
DE cDNA encoding human PRO polypeptide #99.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;

RESULT 145
ID ADA77949 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 146
ID ACF48848 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003104539-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 147
ID ACD09168 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003036131-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 148
ID ACF11961 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003040075-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 149
ID ACF41195 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 150
ID ACF15809 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003044930-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 151
ID ACF16116 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 152
ID ADB17104 standard; cDNA; 766 BP.
DE Human cDNA clone (SeqID 47) encoding the transmembrane PRO protein.
PN US2003050462-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 153
ID ACD31943 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 154
ID ACF18751 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003064452-A1.
PD 03-APR-2003.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
RESULT 155
ID ACF09198 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
RESULT 156
ID ACF78319 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
RESULT 157
ID ACF51918 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003064440-A1.
PD 03-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
RESULT 158
ID ACF26405 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
RESULT 159
ID ACF24198 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
RESULT 160
ID ACF63509 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
RESULT 161
ID ACF50383 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
RESULT 162
ID ACH07854 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
RESULT 163
ID ACF13660 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;

Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 164
ID ACD41586 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
RESULT 165
ID ADA37768 standard; cDNA; 766 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO994.
PN US2003008297-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
RESULT 166
ID ACF31999 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
RESULT 167
ID ACF23277 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
RESULT 168
ID ACF39967 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
RESULT 169
ID ACD45489 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
RESULT 170
ID ACF53146 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
RESULT 171
ID ACF27326 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
RESULT 172
ID ACF45164 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
RESULT 173
ID ACF13660 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;

RESULT 173
ID ACF29782 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 174
ID ACD89858 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 175
ID ACD84639 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #99.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 176
ID ACD98799 standard; cDNA; 766 BP.
DE cDNA encoding human PRO polypeptide #99.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 177
ID ACF77091 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003082717-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 178
ID ACF76784 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 179
ID ACF49769 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003104542-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 180
ID ACF50076 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003104543-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 181
ID ADA21454 standard; cDNA; 766 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO994.
PN US2003054404-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 182
ID ACD09475 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003036127-A1.
PD 20-FEB-2003.

Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 183
ID ACD08554 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003040061-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 184
ID ACH03599 standard; cDNA; 766 BP.
DE Human secreted/transmembrane polypeptide PRO 994 cDNA.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 185
ID ACF12268 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003036130-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 186
ID ACC94776 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 187
ID ACD22495 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 188
ID ACF15195 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003044917-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 189
ID ACC97290 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003044929-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 190
ID ACC92320 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 191
ID ACF13967 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 192
ID ACF14274 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.

PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 193
ID ADA10241 standard; cDNA; 766 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO994.
PN US2003059831-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 194
ID ACF09505 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 195
ID ACD45796 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 196
ID ACD47945 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 197
ID ACD67676 standard; cDNA; 766 BP.
DE cDNA encoding human PRO polypeptide #99.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 198
ID ACF25484 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 199
ID ACF29168 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 200
ID ACD84946 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 201
ID ACD84025 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #99.
PN US2003068758-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 202
ID ACD88016 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 203
ID ACF30703 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 204
ID ACF32306 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 205
ID ACH11966 standard; cDNA; 766 BP.
DE cDNA encoding human PRO polypeptide #99.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 206
ID ACH12273 standard; cDNA; 766 BP.
DE cDNA encoding human PRO polypeptide #99.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 207
ID ADA19909 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 208
ID ACD40665 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003032134-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 209
ID ADB17292 standard; cDNA; 766 BP.
DE Human cDNA clone (SeqID 47) encoding the transmembrane PRO protein.
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 210
ID ADA17785 standard; cDNA; 766 BP.
DE cDNA encoding human PRO994 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;

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RESULT 211
ID ACF18137 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 766; DB 9; Length 766;
  Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 212
ID ACF08584 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 766; DB 9; Length 766;
  Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 213
ID ACF31385 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 766; DB 9; Length 766;
  Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 214
ID ACF52225 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 766; DB 9; Length 766;
  Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 215
ID ACD50094 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 766; DB 9; Length 766;
  Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 216
ID ACF38797 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 766; DB 9; Length 766;
  Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 217
ID ACF26712 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 766; DB 9; Length 766;
  Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 218
ID ACF24812 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 766; DB 9; Length 766;
  Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 219
ID ACF46392 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 766; DB 9; Length 766;
  Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 220
ID ACF27940 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 766; DB 9; Length 766;
  Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 221
ID ACD89244 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 766; DB 9; Length 766;
  Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 222
ID ACF63816 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 766; DB 9; Length 766;
  Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 223
ID ACF60456 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003087374-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 766; DB 9; Length 766;
  Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 224
ID ACH12580 standard; cDNA; 766 BP.
DE cDNA encoding human PRO polypeptide #99.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 766; DB 9; Length 766;
  Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 225
ID ACH10003 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 766; DB 9; Length 766;
  Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 226
ID ACD03858 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003040055-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 766; DB 9; Length 766;
  Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 227
ID ACD10396 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003036164-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 766; DB 9; Length 766;
  Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 228
ID ACD12038 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003040074-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 766; DB 9; Length 766;
  Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 229
ID ACF42423 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
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Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 230
ID ADA27893 standard; cDNA; 766 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO994.
PN US2003054359-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 231
ID ACF18444 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 232
ID ACF02234 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 233
ID ACF21742 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 234
ID ACF10426 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003073169-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 235
ID ACF33878 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 236
ID ACF44840 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 237
ID ACD90472 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 238
ID ACD91085 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 239

ID ACF30396 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 240
ID ACD87095 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 241
ID ACF60149 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 242
ID ACF46699 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003087373-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 243
ID ACF75556 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003096353-A1.
PD 22-MAY-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 244
ID ADA79741 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003073173-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 245
ID ACF17216 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003054458-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 246
ID ACF22970 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 247
ID ACF07970 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 248
ID ACF08277 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

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Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
RESULT 249
ID ACF40581 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
RESULT 250
ID ACF53760 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
RESULT 251
ID ACD47024 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
RESULT 252
ID ACF47927 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
RESULT 253
ID ACF47313 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
RESULT 254
ID ACF46085 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
RESULT 255
ID ACD86174 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
RESULT 256
ID ACF52532 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003082715-A1.
PD 01-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
RESULT 257
ID ACF52839 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003082716-A1.
PD 01-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
RESULT 258
ID ACF17523 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003054460-A1.
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ID ACF64832 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
RESULT 259
ID ACF76477 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
RESULT 260
ID ACF61377 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
RESULT 261
ID ACF61684 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
RESULT 262
ID ACD30715 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003032125-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
RESULT 263
ID ACD31636 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003054454-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
RESULT 264
ID ACD32557 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
RESULT 265
ID ADA20081 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
RESULT 266
ID ACD82113 standard; cDNA; 766 BP.
DE Human secreted/transmembrane polypeptide PRO 994 cDNA.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
RESULT 267
ID ACF17523 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003054460-A1.
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PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 268
ID ADA94473 standard; cDNA; 766 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO994.
PN US2003059832-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 269
ID ACF07356 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 270
ID ACF20514 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 271
ID ACF20821 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 272
ID ACF21128 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 273
ID ACD47638 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 274
ID ACF47620 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 275
ID ACF53453 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 276
ID ACD86788 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;

RESULT 277
ID ACH05036 standard; cDNA; 766 BP.
DE CDNA encoding human PRO polypeptide #99.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 278
ID ACF44533 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 279
ID ADA81468 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 280
ID ACD22188 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003027276-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 281
ID ACD24535 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003044920-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 282
ID ACD39738 standard; cDNA; 766 BP.
DE CDNA encoding human PRO polypeptide #99.
PN US2003027265-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 283
ID ACD40045 standard; cDNA; 766 BP.
DE CDNA encoding human PRO polypeptide #99.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 284
ID ACF13353 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 285
ID ACF03155 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 286
ID ACF78626 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003049783-A1.

PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 287
ID ACF11347 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003073171-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 288
ID ACF50690 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003032121-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 289
ID ACF34185 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 290
ID ACD46410 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 291
ID ACD48252 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 292
ID ACF27633 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 293
ID ACF24505 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 294
ID ACD85560 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 295
ID ACD90165 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;

Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 296
ID ACD83718 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #99.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 297
ID ACF49155 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003104540-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 298
ID ACH07240 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 299
ID ACH07547 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 300
ID ACH08161 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 301
ID ACH11352 standard; cDNA; 766 BP.
DE cDNA encoding human PRO polypeptide #99.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 302
ID ACH11659 standard; cDNA; 766 BP.
DE cDNA encoding human PRO polypeptide #99.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 303
ID ACH10310 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 304
ID ACF01313 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003040059-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 305
ID ACF40888 standard; cDNA; 766 BP.

DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 306
ID ACD24228 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003044918-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
RESULT 307
ID ACD31329 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003032132-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
RESULT 308
ID ACF17830 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 309
ID ADA38698 standard; cDNA; 766 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO994.
PN US2003059780-A1.
PD 27-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
RESULT 310
ID ACF32613 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 311
ID ACF40274 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 312
ID ACF48234 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003064441-A1.
PD 03-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
RESULT 313
ID ACF38183 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 314
ID ACF25119 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;

Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 315
ID ACF27019 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 316
ID ACF29475 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003073174-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
RESULT 317
ID ACD87709 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 318
ID ACF76170 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 319
ID ACF49462 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003104541-A1.
PD 05-JUN-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
RESULT 320
ID ACF43919 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 321
ID ACH06264 standard; cDNA; 766 BP.
DE cDNA encoding human PRO polypeptide #99.
PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 322
ID ACH06571 standard; cDNA; 766 BP.
DE cDNA encoding human PRO polypeptide #99.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 323
ID ADA83266 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 324
ID ACC92627 standard; cDNA; 766 BP.

DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003032133-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 325
ID ACC93241 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003032136-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 326
ID ACF19286 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003036129-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 327
ID ACD12977 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003040053-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 328
ID ACF06435 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003040057-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 329
ID ACC94469 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 330
ID ACC97897 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003044932-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 331
ID ACC94162 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003027270-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 332
ID ACF42116 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 333
ID ACD31022 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003032126-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 334
ID ACD43051 standard; cDNA; 766 BP.
DE cDNA encoding human PRO polypeptide #99.

PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 335
ID ACD43358 standard; cDNA; 766 BP.
DE cDNA encoding human PRO polypeptide #99.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 336
ID ACF14888 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 337
ID ADA92819 standard; cDNA; 766 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO994.
PN US2003060407-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 338
ID ACF01620 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003049738-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 339
ID ACF31692 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 340
ID ACD67369 standard; cDNA; 766 BP.
DE cDNA encoding human PRO polypeptide #99.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 341
ID ACD48559 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 342
ID ACD48866 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 343
ID ACF51304 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 344
ID ACF54067 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 345
ID ACF25791 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 346
ID ACF39104 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 347
ID ACF28861 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 348
ID ACD90778 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 349
ID ACD86481 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 350
ID ACH05343 standard; cDNA; 766 BP.
DE cDNA encoding human PRO polypeptide #99.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 351
ID ACF65139 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 352
ID ADB20309 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003082767-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;

RESULT 353
ID ACF43612 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 354
ID ACH09082 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 355
ID ACH09389 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 356
ID ADA78561 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 357
ID ACF09812 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 358
ID ADA00378 standard; cDNA; 766 BP.
DE Human secreted/transmembrane polypeptide PRO 994 cDNA.
PN US2003027992-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 359
ID ACF50997 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 360
ID ACF23891 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 361
ID ACD88323 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 362
ID ACD88323 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;

ID ACH09696 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 363
ID ACH10617 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 364
ID ACD11424 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003036126-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 365
ID ACC96474 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003044924-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 366
ID ACC98504 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003044927-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 367
ID ACF41809 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003040072-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 368
ID ACF16730 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003040073-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 369
ID ACD32250 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 370
ID ACD30408 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003032124-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 371
ID ACD41279 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;

RESULT 372
ID ACF07663 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 373
ID ACF31078 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 374
ID ACF77398 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 375
ID ACF11040 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003073170-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 376
ID ACF32920 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 377
ID ACF26098 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 378
ID ACD83411 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #99.
PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 379
ID ACF23584 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 380
ID ACF42998 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 381
ID ACF43305 standard; cDNA; 766 BP.

DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 382
ID ACH05957 standard; cDNA; 766 BP.
DE cDNA encoding human PRO polypeptide #99.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 383
ID ACH08775 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 384
ID ACC90369 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003027273-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 385
ID ACF10733 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003036119-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 386
ID ACC93548 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003036120-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 387
ID ACC96167 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 388
ID ACD24842 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003044921-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 389
ID ACF01927 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 390
ID ACF22049 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;

Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 391
ID ACF22663 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 392
ID ACF08891 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 393
ID ACF33227 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 394
ID ACF54681 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 395
ID ACF48541 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 396
ID ACD47331 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 397
ID ACD49173 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003068710-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 398
ID ACF37876 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068686-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 399
ID ACF30089 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003073178-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;

RESULT 400
ID ACD87402 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003068774-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 401
ID ACF61991 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003104538-A1.
PD 05-JUN-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 402
ID ACH10924 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 403
ID ACD10089 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003036158-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 404
ID ACD16814 standard; cDNA; 766 BP.
DE cDNA encoding human PRO polypeptide #99.
PN US2003036151-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 405
ID ACH65449 standard; cDNA; 766 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO994.
PN US2003044806-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 406
ID ACC99111 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003040067-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 407
ID ACF00505 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003054456-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 408
ID ACD40972 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003054482-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 409
ID ACF14581 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003054457-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;

Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 410
ID ACF22356 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003059883-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 411
ID ACF78933 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003049764-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 412
ID ACF11654 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003073177-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 413
ID ADA22380 standard; cDNA; 766 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO994.
PN US2003040473-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 414
ID ACF51611 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003064442-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 415
ID ACF33534 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003064450-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 416
ID ACD49787 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003068731-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 417
ID ACF37569 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068683-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 418
ID ACF28554 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068754-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 419
ID ACD88630 standard; cDNA; 766 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003068681-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 420
ID ACF75249 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003096351-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 421
ID ACF61070 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003096358-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 422
ID ACF44226 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003104556-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 423
ID ACH08468 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 424
ID ACD39439 standard; cDNA; 766 BP.
DE Human cDNA encoding PRO812.
PN US2003017982-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 425
ID ACC93855 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003036122-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 426
ID ACD20960 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 427
ID ACF06742 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003040065-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 428
ID ACD20653 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003044919-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;

RESULT 429
ID ACD22802 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003040077-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 430
ID ACF41502 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003044928-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 431
ID ADA06546 standard; cDNA; 766 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #73.
PN US2003049638-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 432
ID ADA39239 standard; cDNA; 766 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO994.
PN US2003059782-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 433
ID ACF07049 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 434
ID ACF77705 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 435
ID ACD46103 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 436
ID ACF47006 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068757-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 437
ID ACF54374 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 438
ID ACF45778 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068741-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 439
ID ACF45471 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 440
ID ACF38490 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 441
ID ACD89551 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 442
ID ACD85253 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 443
ID ACD85867 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 444
ID ACF75863 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 445
ID ACF60763 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 446
ID ACH05650 standard; cDNA; 766 BP.
DE cDNA encoding human PRO polypeptide #99.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 447
ID ADA82632 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 448
ID ADB85620 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003049735-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 449
ID ADB96265 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #73.
PN US2003054403-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 450
ID ACF55909 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068680-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 766; DB 9; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 451
ID ACF55295 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 452
ID ADB85940 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 453
ID ACF56216 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 454
ID ACF56523 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 455
ID ADB68299 standard; cDNA; 766 BP.
DE Human PRO994 cDNA.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 456
ID ADB68106 standard; cDNA; 766 BP.
DE Human PRO994 cDNA.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 457

ID ACF55602 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
Pred. No. 5.8e-222;
RESULT 458
ID ACF54988 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
Pred. No. 5.8e-222;
RESULT 459
ID ADB90923 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
Pred. No. 5.8e-222;
RESULT 460
ID ADC57737 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #73.
PN US2003027754-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
Pred. No. 5.8e-222;
RESULT 461
ID ADC55101 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #73.
PN US2003045463-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
Pred. No. 5.8e-222;
RESULT 462
ID ADC11968 standard; cDNA; 766 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO994.
PN US2003049681-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
Pred. No. 5.8e-222;
RESULT 463
ID ADC07003 standard; cDNA; 766 BP.
DE Human PRO994 cDNA.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
Pred. No. 5.8e-222;
RESULT 464
ID ADC56390 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #73.
PN US2003064375-A1.
PD 03-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
Pred. No. 5.8e-222;
RESULT 465
ID ADC17182 standard; cDNA; 766 BP.
DE cDNA sequence encoding a PRO polypeptide (SeqID 47).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
Pred. No. 5.8e-222;
RESULT 466
ID ADC07445 standard; cDNA; 766 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO994.
PN US2003068647-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
Pred. No. 5.8e-222;

Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 467
ID ADC11435 standard; cDNA; 766 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO994.
PN US2003069403-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
Pred. No. 5.8e-222;
RESULT 468
ID ADC14880 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
Pred. No. 5.8e-222;
RESULT 469
ID ADC52375 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
Pred. No. 5.8e-222;
RESULT 470
ID ADC14557 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003082546-A1.
PD 01-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
Pred. No. 5.8e-222;
RESULT 471
ID ADD08089 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003068623-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
Pred. No. 5.8e-222;
RESULT 472
ID ADC81914 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #73.
PN US2003083461-A1.
PD 01-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
Pred. No. 5.8e-222;
RESULT 473
ID ADD07556 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
Pred. No. 5.8e-222;
RESULT 474
ID ADC82447 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #73.
PN US2003059833-A1.
PD 27-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
Pred. No. 5.8e-222;
RESULT 475
ID ADD05670 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
Pred. No. 5.8e-222;
RESULT 476
ID ADD08627 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003073090-A1.
PD 17-APR-2003.

Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 477
ID ADD06876 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 478
ID ADC83123 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #73.
PN US2003059783-A1.
PD 27-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 479
ID ADD55230 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #73.
PN US2003077593-A1.
PD 24-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 480
ID ADD36051 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003105298-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 481
ID ADD56188 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #73.
PN US2003077594-A1.
PD 24-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 482
ID ADD54626 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #73.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 483
ID ADE26780 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003087304-A1.
PD 08-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 484
ID ADE26247 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003087305-A1.
PD 08-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 485
ID ADF67184 standard; cDNA; 766 BP.
DE Human PRO994 nucleotide sequence SEQ ID NO:257.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 486
ID ADG01052 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003078387-A1.

PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 487
ID ADG08605 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 488
ID ADG02665 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 489
ID ADG01372 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 490
ID ADF95547 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 491
ID ADF95226 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 492
ID ADG12362 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003207392-A1.
PD 06-NOV-2003.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 493
ID ADH24079 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 494
ID ADH34105 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180858-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 495
ID ADH29938 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 496
ID ADH23909 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180919-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 497
ID ADH09022 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #99.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 498
ID ADG85313 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 499
ID ADH24589 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180907-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 500
ID ADH37445 standard; cDNA; 766 BP.
DE Human secreted and transmembrane protein PRO994 cDNA.
PN US2003181646-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 501
ID ADH02034 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #24.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 502
ID ADH37615 standard; cDNA; 766 BP.
DE Human secreted and transmembrane protein PRO994 cDNA.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 503
ID ADG85653 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 504
ID ADH24249 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 505
ID ADH38543 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003181643-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 506
ID ADG83664 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #24.
PN US2003180794-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 507
ID ADH29472 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 508
ID ADH27588 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 509
ID ADH37785 standard; cDNA; 766 BP.
DE Human secreted and transmembrane protein PRO994 cDNA.
PN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 510
ID ADH37962 standard; cDNA; 766 BP.
DE Human secreted and transmembrane protein PRO994 cDNA.
PN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 511
ID ADH57382 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 512
ID ADH53524 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 513
ID ADH53694 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 514
ID ADH24249 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 766; DB 10; Length 766;
RESULT 515
ID ADH24249 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

RESULT 514
ID ADH52030 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 515
ID ADH49885 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 516
ID ADI25395 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 517
ID ADH90188 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 518
ID ADI25565 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003181669-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 519
ID ADH97739 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 520
ID ADI35438 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #73.
PN US2003050457-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 521
ID ADI03597 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 522
ID ADI11944 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #24.
PN US2003181686-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 523
ID ADH90018 standard; cDNA; 766 BP.

DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003181697-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 524
ID ADH99930 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003049682-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 525
ID ADH98419 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 526
ID ADI11094 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #24.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 527
ID ADI11604 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #24.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 528
ID ADH98249 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 529
ID ADH98589 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003181708-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 530
ID ADH98079 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003181673-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 531
ID ABX78626 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #99.
PN US2003027272-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 532
ID ACA75598 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003032127-A1.
PD 13-FEB-2003.

Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 533
ID ACA71078 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003032112-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 534
ID ACC87606 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003027278-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 535
ID ACC86992 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003036159-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 536
ID ACD04165 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003040070-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 537
ID ABX77878 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #73.
PN US2003027163-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 538
ID ABX80290 standard; DNA; 766 BP.
DE Novel human secreted or transmembrane protein PRO812 DNA.
PN US2002132252-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 539
ID ACA69196 standard; cDNA; 766 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO994.
PN US2003032023-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 540
ID ACA69496 standard; cDNA; 766 BP.
DE cDNA encoding human PRO polypeptide #99.
PN US2003032113-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 541
ID ACA90341 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003036147-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 542
ID ACC89448 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;

RESULT 543
ID ABX90267 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein cDNA, #103.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 544
ID ACA98239 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 545
ID ACA93881 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 546
ID ACD15274 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 547
ID ACD08861 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 548
ID ACC96781 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 549
ID ACF15502 standard; cDNA; 766 BP.
DE Human secreted polypeptide PRO994-encoding cDNA, SEQ ID NO:197.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 550
ID ABX64113 standard; cDNA; 766 BP.
DE cDNA encoding human PRO994 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH LTD.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 551
ID ACA72869 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #99.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 552
ID ACD03041 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;

RESULT 553
ID ACD01856 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 554
ID ACA92048 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 555
ID ADI05067 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180848-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 556
ID ADI03417 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003181654-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 557
ID ADI04812 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003181657-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 558
ID ADH78266 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #24.
PN US2003181668-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 559
ID ADI19610 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003181676-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 560
ID ADH90358 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003181699-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 561
ID ADI03077 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003181653-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 562
ID ADH77926 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #24.

PN US2003181666-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 563
ID ADH97909 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003181674-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 564
ID ADI01294 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003190669-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 565
ID ADI01989 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003181652-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 566
ID ADI03247 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003181655-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 567
ID ADI11434 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #24.
PN US2003181681-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 568
ID ADI02336 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003181650-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 569
ID ADI11774 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #24.
PN US2003181685-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 570
ID ADI05411 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003190716-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 571
ID ADH79483 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003191290-A1.

PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 572
ID ADI19440 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003181675-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 573
ID ADI05241 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003181677-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 574
ID ADH79653 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003191288-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 575
ID ADI01479 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003181678-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 576
ID ADI01649 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003181679-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 577
ID ADI01819 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003181680-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 578
ID ADH79823 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003191289-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 579
ID ADI04641 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003171550-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 580
ID ADI02777 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003181651-A1.
PD 25-SEP-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 581
ID ADH78096 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #24.
PN US2003181667-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 582
ID ADI25735 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003181670-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 583
ID ADI25905 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003181671-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 584
ID ADK65417 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003073821-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 585
ID ADH98759 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 586
ID ADH80000 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 10; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 587
ID ADL32803 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003207396-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 11; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 588
ID ADM30337 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003073813-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 11; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 589
ID ADL93731 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 766; DB 11; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 590
ID ADC52185 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003130483-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 591
ID ADE74334 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003211572-A1.
PD 13-NOV-2003.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 592
ID ADE74946 standard; cDNA; 766 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #99.
PN US2003211574-A1.
PD 13-NOV-2003.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 593
ID ADF35383 standard; cDNA; 766 BP.
DE CDNA encoding human PRO994 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 594
ID ADG11633 standard; cDNA; 766 BP.
DE CDNA encoding human PRO994 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 595
ID ADF96159 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003215909-A1.
PD 20-NOV-2003.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 596
ID ADG04430 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003215912-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 597
ID ADG00590 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003215911-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 598
ID ADH06617 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180852-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 599
ID ADH06447 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.

PN US2003180853-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 600
ID ADG68868 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180855-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 601
ID ADH27758 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180912-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 602
ID ADH25099 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180913-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 603
ID ADH33731 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #24.
PN US2003181645-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 604
ID ADG82846 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #99.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 605
ID ADH02374 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #24.
PN US2003180839-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 606
ID ADH07981 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180845-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 607
ID ADG69378 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180846-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 608
ID ADH39199 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180917-A1.

PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 609
ID ADH26127 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 610
ID ADG83939 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #24.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 611
ID ADH19503 standard; cDNA; 766 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO994.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 612
ID ADG85483 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003166848-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 613
ID ADH06277 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 614
ID ADH30107 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 615
ID ADH24419 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 616
ID ADH33096 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #99.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 617
ID ADG69548 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180844-A1.
PD 25-SEP-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 618
ID ADH07811 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 619
ID ADG85823 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 620
ID ADH39369 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 621
ID ADH33561 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #24.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 622
ID ADH33901 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #24.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 623
ID ADH01111 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #24.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 624
ID ADG69718 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 625
ID ADH20996 standard; cDNA; 766 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO994.
PN US2003224358-A1.
PD 04-DEC-2003.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 626
ID ADH02204 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #24.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;

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Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 627
ID ADG69208 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 628
ID ADG85993 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 629
ID ADH24929 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180909-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 630
ID ADH39546 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 631
ID ADH20036 standard; cDNA; 766 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO994.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 632
ID ADH02544 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #24.
PN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 633
ID ADG69038 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 634
ID ADH07641 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 635
ID ADG86163 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 636
ID ADH24759 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 637
ID ADH25807 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 638
ID ADH38373 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 639
ID ADH57212 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003181642-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 640
ID ADH52200 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 641
ID ADH49566 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 642
ID ADH90528 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003181700-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 643
ID ADI11264 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #24.
PN US2003181683-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 644
ID ADH98929 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003190698-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 645
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ID ADI02159 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003190699-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 646
ID ADH90698 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 647
ID ADJ54835 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #99.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 648
ID ADJ98573 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003187197-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 649
ID ADJ98743 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 650
ID ADH78902 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 651
ID ADJ99136 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 652
ID ADJ99306 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 653
ID ADJ98924 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 654
ID ADH79072 standard; cDNA; 766 BP.

DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003181702-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 655
ID ADK00932 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #24.
PN US2003186407-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 656
ID ADK14453 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 657
ID ADJ64606 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #99.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 658
ID ADM31502 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 659
ID ADM36549 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 660
ID ADM40354 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 661
ID ADM80902 standard; cDNA; 766 BP.
DE Human PRO polynucleotide #24.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 662
ID ADN37962 standard; cDNA; 766 BP.
DE Novel human secreted and transmembrane protein PRO994 cDNA.
PN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 766; DB 12; Length 766;
Best Local Similarity 100.0%; Pred. No. 5.8e-222;
RESULT 663
ID AAK88578 standard; cDNA; 734 BP.
DE Human digestive system antigen coding sequence SEQ ID NO: 894.

PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 56.1%; Score 429.6; DB 4; Length 734;
Best Local Similarity 98.7%; Pred. No. 9.6e-120;
RESULT 664
ID AAS37892 standard; cDNA; 351 BP.
DE Novel human diagnostic and therapeutic gene #950.
PN WO200166753-A2.
PD 13-SEP-2001.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 34.5%; Score 264.2; DB 4; Length 351;
Best Local Similarity 91.0%; Pred. No. 1.2e-69;
RESULT 665
ID AAF98695 standard; DNA; 286 BP.
DE Human ovarian cancer cell expressed sequence 10793.
PN WO200118542-A2.
PD 15-MAR-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 30.2%; Score 231.4; DB 5; Length 286;
Best Local Similarity 99.6%; Pred. No. 1.1e-59;
RESULT 666
ID AAS38101 standard; cDNA; 378 BP.
DE Novel human diagnostic and therapeutic gene #1159.
PN WO200166753-A2.
PD 13-SEP-2001.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 19.4%; Score 148.6; DB 4; Length 378;
Best Local Similarity 89.4%; Pred. No. 1.7e-34;
RESULT 667
ID ABS72969 standard; cDNA; 106 BP.
DE Human gene trapped sequence (GTS) #929.
PN US2002095031-A1.
PD 18-JUL-2002.
PA (NEHL/) NEHLS M C.
PA (ZAMB/) ZAMBROWICZ B.
PA (SAND/) SANDS A T.
Query Match 9.0%; Score 69; DB 6; Length 106;
Best Local Similarity 88.7%; Pred. No. 1.5e-10;
RESULT 668
ID ABN47584 standard; DNA; 60 BP.
DE Human spliced transcript detection oligonucleotide SEQ ID NO:20332.
PN WO200210449-A2.
PD 07-FEB-2002.
PA (COMP-) COMPUGEN INC.
Query Match 7.8%; Score 60; DB 6; Length 60;
Best Local Similarity 100.0%; Pred. No. 6.2e-08;
RESULT 669
ID ADA71938 standard; DNA; 2000 BP.
DE Rice gene, SEQ ID 5263.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 5.7%; Score 43.4; DB 8; Length 2000;
Best Local Similarity 10.6%; Pred. No. 0.035;
RESULT 670
ID ACH17322 standard; cDNA; 404 BP.
DE Human adult heart cDNA #1636.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 5.1%; Score 39.4; DB 9; Length 404;
Best Local Similarity 52.8%; Pred. No. 0.27;
RESULT 671
ID ACH15938 standard; cDNA; 410 BP.
DE Human adult heart cDNA #252.
PN US2003073623-A1.

PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 5.1%; Score 39.4; DB 9; Length 410;
Best Local Similarity 52.8%; Pred. No. 0.28;
RESULT 672
ID ACC44333 standard; DNA; 3447 BP.
DE Gene encoding human structural and cytoskeletal associated protein #37.
PN WO2003031940-A2.
PD 17-APR-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 5.1%; Score 39.4; DB 8; Length 3447;
Best Local Similarity 52.8%; Pred. No. 0.75;
RESULT 673
ID ADD14717 standard; cDNA; 8034 BP.
DE Human src biomarker polynucleotide SEQ ID NO:111.
PN WO2003062395-A2.
PD 31-JUL-2003.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 5.1%; Score 39.4; DB 10; Length 8034;
Best Local Similarity 52.8%; Pred. No. 1.1;
RESULT 674
ID ADI24481 standard; cDNA; 8034 BP.
DE Human modifier of Chk1 (MCHK) encoding cDNA SEQ ID NO:31.
PN WO2004004785-A1.
PD 15-JAN-2004.
PA (EXEL-) EXELIXIS INC.
Query Match 5.1%; Score 39.4; DB 12; Length 8034;
Best Local Similarity 52.8%; Pred. No. 1.1;
RESULT 675
ID AAS35237 standard; cDNA; 447 BP.
DE Human cardiovascular system antigen cDNA polynucleotide SEQ ID NO 122.
PN WO200155321-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.1%; Score 39; DB 4; Length 447;
Best Local Similarity 52.2%; Pred. No. 0.38;
RESULT 676
ID ADE45316 standard; cDNA; 447 BP.
DE Human cardiovascular system related polynucleotide #112.
PN US2003059908-A1.
PD 27-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.1%; Score 39; DB 10; Length 447;
Best Local Similarity 52.2%; Pred. No. 0.38;
RESULT 677
ID ADC93538 standard; DNA; 369 BP.
DE E. faecium DNA sequence SEQ ID 3165.
PN US6583275-B1.
PD 24-JUN-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.8%; Score 36.4; DB 10; Length 369;
Best Local Similarity 51.2%; Pred. No. 2.1;
RESULT 678
ID ABN26464 standard; cDNA; 427 BP.
DE Human ORFX polynucleotide sequence SEQ ID NO:21405.
PN WO200192523-A2.
PD 06-DEC-2001.
PA (CURA-) CURAGEN CORP.
Query Match 4.7%; Score 36.2; DB 6; Length 427;
Best Local Similarity 46.0%; Pred. No. 2.6;
RESULT 679
ID AAX13287 standard; DNA; 3274 BP.
DE Enterococcus faecalis genome contig SEQ ID NO:350.
PN WO9850555-A2.
PD 12-NOV-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 36.2; DB 2; Length 3274;
Best Local Similarity 51.6%; Pred. No. 6.8;
RESULT 680

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ID ABS99082 standard; DNA; 3274 BP.
DE Enterococcus faecalis contig sequence #350.
PN US2002120116-A1.
PD 29-AUG-2002.
PA (KUNS/) KUNSCH C A.
PA (DILL/) DILLON P J.
PA (BARA/) BARASH S.
Query Match
Best Local Similarity 4.7%; Score 36.2; DB 6; Length 3274;
RESULT 681
ID ABL33154 standard; DNA; 5807 BP.
DE Human immune system associated gene SEQ ID NO: 1127.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 4.7%; Score 36; DB 6; Length 5807;
RESULT 682
ID ABX57335 standard; DNA; 540 BP.
DE Arabidopsis thaliana polynucleotide #687.
PN US2002040489-A1.
PD 04-APR-2002.
PA (GORL/) GORLACH J.
PA (ANYV/) AN Y.
PA (HAMI/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (RAIN/) RAINES T M.
PA (YUYV/) YU Y.
PA (RAME/) RAMEAKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHEW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
PA (KRIC/) KRICKER M.
PA (SLAT/) SLATER T.
PA (DAVI/) DAVIS K R.
PA (ALLE/) ALLEN K.
PA (HOFF/) HOFFMAN N.
PA (HURB/) HURBAN P.
Query Match
Best Local Similarity 4.6%; Score 35; DB 10; Length 540;
RESULT 683
ID ADP84152 standard; DNA; 42347 BP.
DE Human CAL25 genomic DNA extracellular repeat sequence SeqID 2.
Query Match
Best Local Similarity 4.6%; Score 35; DB 12; Length 42347;
RESULT 684
ID AAC84840 standard; cDNA; 1809 BP.
DE Sunflower berberine bridge enzyme (BBE) encoding cDNA.
PN WO200078983-A2.
PD 28-DEC-2000.
PA (PION-) PIONEER HI-BRED INT INC.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 4.5%; Score 34.8; DB 5; Length 1809;
RESULT 685
ID AAS86817 standard; cDNA; 2926 BP.
DE DNA encoding novel human diagnostic protein #22621.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 4.5%; Score 34.8; DB 5; Length 2926;
RESULT 686
ID AAS90969 standard; cDNA; 2926 BP.
DE DNA encoding novel human diagnostic protein #26773.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 4.5%; Score 34.8; DB 5; Length 2926;
RESULT 687
Query Match
Best Local Similarity 4.5%; Score 34.8; DB 10; Length 110000;
RESULT 688
ID ACF65382 standard; DNA; 243072 BP.
DE Photorhabdus luminescens nucleotide sequence #35.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP ) INST PASTEUR.
PA (CNRS ) CNRS CENT NAT RECH SCI.
Query Match
Best Local Similarity 4.5%; Score 34.8; DB 10; Length 243072;
RESULT 689
ID AAX84332 standard; DNA; 5059 BP.
DE Stealth virus nucleic acid clone, SEQ ID NO: 24.
Query Match
Best Local Similarity 4.5%; Score 34.6; DB 2; Length 5059;
RESULT 690
ID ABL32051 standard; DNA; 16545 BP.
DE Human immune system associated gene SEQ ID NO: 24.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 4.5%; Score 34.6; DB 6; Length 16545;
RESULT 691
ID ABZ32482 standard; DNA; 1413 BP.
DE Candida albicans essential gene SEQ ID NO 6769.
PN WO200253728-A2.
PD 11-JUL-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 4.5%; Score 34.4; DB 6; Length 1413;
RESULT 692
ID AAS96692 standard; DNA; 8880 BP.
DE Arabidopsis DMT2 (1DMT2) DNA.
PN WO200180626-A1.
PD 01-NOV-2001.
PA (REGC ) UNIV CALIFORNIA.
Query Match
Best Local Similarity 4.5%; Score 34.2; DB 6; Length 8880;
RESULT 693
ID ADM39541 standard; DNA; 8880 BP.
DE DMT polynucleotide #7.
PN US2003135890-A1.
PD 17-JUL-2003.
PA (FISC/) FISCHER R.
PA (CHOI/) CHOI Y.
PA (HANN/) HANNON M.
PA (OKAM/) OKAMURO J.
PA (TATA/) TATARINOVA T.
Query Match
Best Local Similarity 4.5%; Score 34.2; DB 11; Length 8880;
RESULT 694
ID AAK70445 standard; DNA; 18949 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25257.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 4.5%; Score 34.2; DB 4; Length 18949;
RESULT 695
ID AAX20253 standard; DNA; 26811 BP.
DE Borrelia burgdorferi polynucleotide sequence #6.
PN WO9858943-A1.
PD 30-DEC-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (MEDI-) MEDIMMUNE INC.
Query Match
Best Local Similarity 4.5%; Score 34.2; DB 2; Length 26811;
RESULT 696
Query Match
Best Local Similarity 4.5%; Score 34.2; DB 6; Length 110000;
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RESULT 697
ID ABQ76613 standard; cDNA; 24142 BP.
DE C. albicans BAX-associated cDNA fragment SEQ ID 651.
PN WO200264766-A2.
PD 22-AUG-2002.
PA (JANC) JANSSEN PHARM NV.
Query Match 4.4%; Score 34; DB 6; Length 24142;
Best Local Similarity 51.3%; Pred. No. 81;
RESULT 698
ID ADO47193 standard; DNA; 200000 BP.
DE DNA sequence of a human immunoglobulin heavy chain variable region.
PN WO2004029249-A1.
PD 08-APR-2004.
PA (CENT-) CENTENARY INST CANCER MEDICINE & CELL BI.
Query Match 4.4%; Score 34; DB 12; Length 200000;
Best Local Similarity 57.5%; Pred. No. 2.2e+02;
RESULT 699
ID AAI18674 standard; DNA; 575 BP.
DE Probe #8607 for gene expression analysis in human cervical cell sample.
PN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 4.4%; Score 33.8; DB 4; Length 575;
Best Local Similarity 55.6%; Pred. No. 16;
RESULT 700
ID ABA63673 standard; DNA; 575 BP.
DE Human foetal liver single exon nucleic acid probe #11978.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 4.4%; Score 33.8; DB 4; Length 575;
Best Local Similarity 55.6%; Pred. No. 16;
RESULT 701
ID AAI43787 standard; DNA; 575 BP.
DE Probe #12473 used to measure gene expression in human placenta sample.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 4.4%; Score 33.8; DB 4; Length 575;
Best Local Similarity 55.6%; Pred. No. 16;
RESULT 702
ID AAK37911 standard; DNA; 575 BP.
DE Human bone marrow expressed single exon probe SEQ ID NO: 12468.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 4.4%; Score 33.8; DB 4; Length 575;
Best Local Similarity 55.6%; Pred. No. 16;
RESULT 703
ID AAK12190 standard; DNA; 575 BP.
DE Human brain expressed single exon probe SEQ ID NO: 12181.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 4.4%; Score 33.8; DB 4; Length 575;
Best Local Similarity 55.6%; Pred. No. 16;
RESULT 704
ID ABS37535 standard; DNA; 575 BP.
DE Human liver single exon probe, SEQ ID NO 12525.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 4.4%; Score 33.8; DB 4; Length 575;
Best Local Similarity 55.6%; Pred. No. 16;
RESULT 705
ID ABS11910 standard; DNA; 575 BP.
DE Human genome-derived single exon probe from lung SEQ ID NO 11901.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 4.4%; Score 33.8; DB 6; Length 575;
Best Local Similarity 55.6%; Pred. No. 16;
RESULT 706

ID ACC00411 standard; cDNA; 1088 BP.
DE Human cell adhesion and extracellular matrix protein, CADECM-20, DNA.
PN WO2003027230-A2.
PD 03-APR-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 4.4%; Score 33.6; DB 8; Length 1088;
Best Local Similarity 63.8%; Pred. No. 25;
RESULT 707
ID ABQ67033 standard; DNA; 17970 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 63.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.4%; Score 33.6; DB 6; Length 17970;
Best Local Similarity 44.8%; Pred. No. 94;
RESULT 708
ID ABQ67033 standard; DNA; 17970 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 63.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.4%; Score 33.6; DB 6; Length 110000;
Best Local Similarity 49.4%; Pred. No. 2.2e+02;
RESULT 709
ID ADL13512 standard; DNA; 178870 BP.
DE Osteoarthritis-associated polymorphic nucleotide #44.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 4.4%; Score 33.6; DB 10; Length 178870;
Best Local Similarity 55.0%; Pred. No. 2.7e+02;
RESULT 710
ID ABN67938 standard; DNA; 912 BP.
DE Streptococcus polynucleotide SEQ ID NO 3789.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 4.4%; Score 33.4; DB 6; Length 912;
Best Local Similarity 53.4%; Pred. No. 27;
RESULT 711
ID AAS61095 standard; DNA; 5975 BP.
DE Human gene regulation-associated gene oligonucleotide #50.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.4%; Score 33.4; DB 6; Length 5975;
Best Local Similarity 53.4%; Pred. No. 64;
RESULT 712
ID AAS46550 standard; DNA; 6558 BP.
DE Tumour suppressor gene derived chemically modified sequence #272.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.4%; Score 33.4; DB 4; Length 6558;
Best Local Similarity 48.7%; Pred. No. 67;
RESULT 713
ID ADB54160 standard; DNA; 6558 BP.
DE Pretreated genomic DNA region 84.
PN WO2003072821-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.4%; Score 33.4; DB 10; Length 6558;
Best Local Similarity 48.7%; Pred. No. 67;
RESULT 714
ID ADB54288 standard; DNA; 6558 BP.
DE Pretreated genomic DNA region 212.
PN WO2003072821-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.4%; Score 33.4; DB 10; Length 6558;
Best Local Similarity 48.7%; Pred. No. 67;
RESULT 715
ID ADC87618 standard; DNA; 58366 BP.
DE Human GPCR related polynucleotide SEQ ID NO:2071.
PN EPI270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.

PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 4.4%; Score 33.4; DB 10; Length 58366;
Best Local Similarity 47.0%; Pred. No. 1.9e+02;
RESULT 716
ID AAH15410 standard; cDNA; 1391 BP.
DE Human cDNA sequence SEQ ID NO:13620.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 4.3%; Score 33; DB 4; Length 1391;
Best Local Similarity 51.7%; Pred. No. 43;
RESULT 717
ID ABZ13052 standard; DNA; 1602 BP.
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 857.
PN WO200216655-A2.
PD 28-FEB-2002.
PA (SCRI) SCRIPPS RES INST.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 4.3%; Score 33; DB 6; Length 1602;
Best Local Similarity 49.2%; Pred. No. 46;
RESULT 718
ID AAC46279 standard; DNA; 1971 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 49562.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.3%; Score 33; DB 3; Length 1971;
Best Local Similarity 49.2%; Pred. No. 51;
RESULT 719
ID ADA71938 standard; DNA; 2000 BP.
DE Rice gene, SEQ ID 5263.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 4.3%; Score 33; DB 8; Length 2000;
Best Local Similarity 9.2%; Pred. No. 51;
RESULT 720
ID ADP65597 standard; DNA; 2001 BP.
DE Human, Similar to collagen, type V, alpha 2, clone DNA.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match 4.3%; Score 33; DB 11; Length 2001;
Best Local Similarity 45.5%; Pred. No. 51;
RESULT 721
ID ADP65797 standard; DNA; 2001 BP.
DE Human, Similar to collagen, type V, alpha 2, clone DNA.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match 4.3%; Score 33; DB 11; Length 2001;
Best Local Similarity 45.5%; Pred. No. 51;
RESULT 722
ID AAH54098 standard; DNA; 3103 BP.
DE S. epidermidis genomic polynucleotide sequence SEQ ID NO:3462.
PN WO200134809-A2.
PD 17-MAY-2001.
PA (GLAX) GLAXO GROUP LTD.
Query Match 4.3%; Score 33; DB 4; Length 3103;
Best Local Similarity 55.8%; Pred. No. 63;
RESULT 723
ID AAH54877 standard; DNA; 3438 BP.
DE S. epidermidis genomic polynucleotide sequence SEQ ID NO:4241.
PN WO200134809-A2.
PD 17-MAY-2001.
PA (GLAX) GLAXO GROUP LTD.
Query Match 4.3%; Score 33; DB 4; Length 3438;
Best Local Similarity 55.8%; Pred. No. 66;
RESULT 724
ID AAH54633 standard; DNA; 3463 BP.
DE S. epidermidis genomic polynucleotide sequence SEQ ID NO:3997.
PN WO200134809-A2.
PD 17-MAY-2001.
PA (GLAX) GLAXO GROUP LTD.

Query Match 4.3%; Score 33; DB 4; Length 3463;
Best Local Similarity 55.8%; Pred. No. 66;
RESULT 725
ID ADP65055 standard; DNA; 6217 BP.
DE Human collagen, type V, alpha 2 (COL5A2) DNA sequence.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match 4.3%; Score 33; DB 11; Length 6217;
Best Local Similarity 45.5%; Pred. No. 87;
RESULT 726
ID ADP65717 standard; DNA; 6217 BP.
DE Human collagen, type V, alpha 2 (COL5A2) DNA.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match 4.3%; Score 33; DB 11; Length 6217;
Best Local Similarity 45.5%; Pred. No. 87;
RESULT 727
ID ABL15172 standard; cDNA; 9263 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 39998.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.3%; Score 33; DB 4; Length 9263;
Best Local Similarity 47.0%; Pred. No. 1e+02;
RESULT 728
ID AAS29831 standard; DNA; 32205 BP.
DE Human cytoskeletal element-related polypeptide encoding genomic DNA #18.
PN WO200155168-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.3%; Score 33; DB 4; Length 32205;
Best Local Similarity 51.0%; Pred. No. 1.9e+02;
RESULT 729
ID AAS33426 standard; DNA; 32205 BP.
DE DNA encoding human secreted protein, Seq ID No 709.
PN WO200155326-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.3%; Score 33; DB 4; Length 32205;
Best Local Similarity 51.0%; Pred. No. 1.9e+02;
RESULT 730
ID AAK85853 standard; DNA; 39969 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40665.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.3%; Score 33; DB 4; Length 39969;
Best Local Similarity 51.0%; Pred. No. 2.1e+02;
RESULT 731
ID ADL15091 standard; DNA; 125729 BP.
DE Human PHKBPI pseudogene DNA for cancer treatment.
PN WO2003068268-A2.
PD 21-AUG-2003.
PA (BIOI-) BIOINVENT INT AB.
Query Match 4.3%; Score 33; DB 10; Length 125729;
Best Local Similarity 51.7%; Pred. No. 3.5e+02;
RESULT 732
ID ADD50651 standard; DNA; 142299 BP.
DE BAC sequence #2 containing hCMT DNA.
PN US2003114399-A1.
PD 19-JUN-2003.
PA (BLAK/) BLAKELY R D.
PA (APPA/) APPARSUNDARAM S.
PA (FERG/) FERGUSON S.
Query Match 4.3%; Score 33; DB 10; Length 142299;
Best Local Similarity 43.3%; Pred. No. 3.7e+02;
RESULT 733
ID AAK74680 standard; DNA; 8981 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:29492.
PN WO200157182-A2.
PD 09-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.3%; Score 32.8; DB 4; Length 8981;
Best Local Similarity 44.5%; Pred. No. 1.2e+02;
RESULT 734
ID AAQ10613 standard; DNA; 15672 BP.
DE Rianodin receptor gene.
PN JP03011098-A.
PD 18-JAN-1991.
PA (MITU) MITSUBISHI KASEI CORP.
Query Match 4.3%; Score 32.8; DB 2; Length 15672;
Best Local Similarity 58.0%; Pred. No. 1.5e+02;
RESULT 735
ID AAK96119 standard; DNA; 401 BP.
DE Human neuregulin gene single nucleotide polymorphism SNP8NRG997541.
PN WO200164876-A2.
PD 07-SEP-2001.
PA (DECO-) DECODE GENETICS EHF.
Query Match 4.3%; Score 32.6; DB 4; Length 401;
Best Local Similarity 63.3%; Pred. No. 32;
RESULT 736
ID AAK97612 standard; DNA; 401 BP.
DE Human neuregulin gene single nucleotide polymorphism SNP8NRG997541.
PN WO200164877-A2.
PD 07-SEP-2001.
PA (DECO-) DECODE GENETICS EHF.
Query Match 4.3%; Score 32.6; DB 4; Length 401;
Best Local Similarity 63.3%; Pred. No. 32;
RESULT 737
ID ABT00889 standard; DNA; 401 BP.
DE Human neuregulin-1-associated gene 1 fragment SEQ ID NO: 918.
PN US2002045577-A1.
PD 18-APR-2002.
PA (DECO-) DECODE GENETICS EHF.
Query Match 4.3%; Score 32.6; DB 6; Length 401;
Best Local Similarity 63.3%; Pred. No. 32;
RESULT 738
ID ABT02382 standard; DNA; 401 BP.
DE Human neuregulin-1-associated gene 1 fragment SEQ ID NO: 918.
PN US2002094954-A1.
PD 18-JUL-2002.
PA (DECO-) DECODE GENETICS EHF.
Query Match 4.3%; Score 32.6; DB 6; Length 401;
Best Local Similarity 63.3%; Pred. No. 32;
RESULT 739
ID ABZ16774 standard; DNA; 2000 BP.
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 4579.
PN WO200216655-A2.
PD 28-FEB-2002.
PA (SCRI) SCRIPPS RES INST.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 4.3%; Score 32.6; DB 6; Length 2000;
Best Local Similarity 49.7%; Pred. No. 67;
RESULT 740
ID ABN79830 standard; DNA; 2595 BP.
DE Fungal ZBC gene sequence #67.
PN WO200224865-A2.
PD 28-MAR-2002.
PA (MICR-) MICROBIA INC.
Query Match 4.3%; Score 32.6; DB 6; Length 2595;
Best Local Similarity 58.9%; Pred. No. 76;
RESULT 741
ID ABN79831 standard; DNA; 2595 BP.
DE Fungal ZBC gene sequence #68.
PN WO200224865-A2.
PD 28-MAR-2002.
PA (MICR-) MICROBIA INC.
Query Match 4.3%; Score 32.6; DB 6; Length 2595;
Best Local Similarity 58.9%; Pred. No. 76;
RESULT 742
ID AAS95264 standard; DNA; 2897 BP.
DE Long terminal repeat (LTR) retrotransposon #15.
PN WO200181598-A2.
PD 01-NOV-2001.

PA (JANC) JANSSEN PHARM NV.
Query Match 4.3%; Score 32.6; DB 6; Length 2897;
Best Local Similarity 48.2%; Pred. No. 80;
RESULT 743
ID ABL12604 standard; cDNA; 4718 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 32294.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.3%; Score 32.6; DB 4; Length 4718;
Best Local Similarity 52.6%; Pred. No. 1e+02;
RESULT 744
Query Match 4.3%; Score 32.6; DB 4; Length 110000;
Best Local Similarity 63.3%; Pred. No. 4.4e+02;
RESULT 745
Query Match 4.3%; Score 32.6; DB 4; Length 110000;
Best Local Similarity 63.3%; Pred. No. 4.4e+02;
RESULT 746
Query Match 4.3%; Score 32.6; DB 5; Length 110000;
Best Local Similarity 49.1%; Pred. No. 4.4e+02;
RESULT 747
Query Match 4.3%; Score 32.6; DB 6; Length 110000;
Best Local Similarity 63.3%; Pred. No. 4.4e+02;
RESULT 748
Query Match 4.3%; Score 32.6; DB 6; Length 110000;
Best Local Similarity 63.3%; Pred. No. 4.4e+02;
RESULT 749
Query Match 4.3%; Score 32.6; DB 12; Length 110000;
Best Local Similarity 63.3%; Pred. No. 4.4e+02;
RESULT 750
ID ABV12272 standard; cDNA; 415 BP.
DE Human prostate expression marker cDNA 12263.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.2%; Score 32.4; DB 5; Length 415;
Best Local Similarity 54.1%; Pred. No. 37;
RESULT 751
ID ABV42340 standard; cDNA; 459 BP.
DE Human prostate expression marker cDNA 42331.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.2%; Score 32.4; DB 5; Length 459;
Best Local Similarity 54.1%; Pred. No. 39;
RESULT 752
ID ABV33417 standard; cDNA; 459 BP.
DE Human prostate expression marker cDNA 33408.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.2%; Score 32.4; DB 5; Length 459;
Best Local Similarity 54.1%; Pred. No. 39;
RESULT 753
ID ABV50091 standard; cDNA; 587 BP.
DE Human prostate expression marker cDNA 50082.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.2%; Score 32.4; DB 5; Length 587;
Best Local Similarity 49.4%; Pred. No. 44;
RESULT 754
ID ADR01578 standard; DNA; 746 BP.
DE A. gossypii genomic DNA PAG1232RP.
PN US6239264-B1.
PD 29-MAY-2001.
PA (SYNG-) SYNGENTA PARTICIPATIONS AG.
Query Match 4.2%; Score 32.4; DB 2; Length 746;
Best Local Similarity 56.4%; Pred. No. 49;
RESULT 755
ID AAZ29420 standard; cDNA; 804 BP.
DE Chenopodium rubrum CDK11 encoding cDNA.
PN WO9964599-A1.

PD 16-DEC-1999.
PA (MIAC) AGRIC & AGRI-FOOD CANADA.
PA (UYSA-) UNIV SASKATCHEWAN TECHNOLOGIES INC.
PA (CANA) NAT RES COUNCIL CANADA.
Query Match 4.2%; Score 32.4; DB 3; Length 804;
Best Local Similarity 46.8%; Pred. No. 51;
RESULT 756
ID AAD40768 standard; cDNA; 804 BP.
DE Chenopodium rubrum ICDK cDNA.
PN WO200250292-A2.
PD 27-JUN-2002.
PA (MIAC) CANADA MIN AGRIC & AGRI-FOOD CANADA.
PA (UYSA-) UNIV SASKATCHEWAN TECHNOLOGIES INC.
Query Match 4.2%; Score 32.4; DB 6; Length 804;
Best Local Similarity 46.8%; Pred. No. 51;
RESULT 757
ID ABL32274 standard; DNA; 6247 BP.
DE Human immune system associated gene SEQ ID NO: 247.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.2%; Score 32.4; DB 6; Length 6247;
Best Local Similarity 47.9%; Pred. No. 1.3e+02;
RESULT 758
ID ABK28222 standard; DNA; 11394 BP.
DE DNA transcription associated complementary genomic DNA #48.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.2%; Score 32.4; DB 6; Length 11394;
Best Local Similarity 51.4%; Pred. No. 1.8e+02;
RESULT 759
Query Match 4.2%; Score 32.4; DB 10; Length 110000;
Best Local Similarity 52.2%; Pred. No. 5e+02;
RESULT 760
Query Match 4.2%; Score 32.4; DB 10; Length 110000;
Best Local Similarity 56.6%; Pred. No. 5e+02;
RESULT 761
ID ACF65380 standard; DNA; 210710 BP.
DE Photorhabdus luminescens nucleotide sequence #33.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 4.2%; Score 32.4; DB 10; Length 210710;
Best Local Similarity 56.6%; Pred. No. 6.8e+02;
RESULT 762
ID AAC01084 standard; cDNA; 414 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 1082.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Query Match 4.2%; Score 32.2; DB 3; Length 414;
Best Local Similarity 56.0%; Pred. No. 43;
RESULT 763
ID ABA63245 standard; DNA; 504 BP.
DE Human foetal liver single exon nucleic acid probe #11550.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 4.2%; Score 32.2; DB 4; Length 504;
Best Local Similarity 52.6%; Pred. No. 47;
RESULT 764
ID ABK53968 standard; cDNA; 537 BP.
DE Human head and neck tumour cDNA, SEQ ID No 163.
PN WO200212329-A2.
PD 14-FEB-2002.
PA (CORI-) CORIXA CORP.
Query Match 4.2%; Score 32.2; DB 6; Length 537;
Best Local Similarity 50.3%; Pred. No. 48;
RESULT 765
ID AAC65137 standard; DNA; 855 BP.
DE Adipocyte complement related protein homologue zacrp2 degenerate DNA.

PD WO200063376-A1.
PD 26-OCT-2000.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 4.2%; Score 32.2; DB 3; Length 855;
Best Local Similarity 26.4%; Pred. No. 60;
RESULT 766
ID ADM66430 standard; DNA; 855 BP.
DE Degenerate DNA encoding human zacrp2.
PN US6620909-B1.
PD 16-SEP-2003.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 4.2%; Score 32.2; DB 11; Length 855;
Best Local Similarity 26.4%; Pred. No. 60;
RESULT 767
ID ADL26865 standard; DNA; 855 BP.
DE Human zacrp2 degenerate DNA.
PN US2004024187-A1.
PD 05-FEB-2004.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 4.2%; Score 32.2; DB 12; Length 855;
Best Local Similarity 26.4%; Pred. No. 60;
RESULT 768
ID AAK69219 standard; DNA; 1390 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24031.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.2%; Score 32.2; DB 4; Length 1390;
Best Local Similarity 50.3%; Pred. No. 75;
RESULT 769
ID ABV25179 standard; cDNA; 1522 BP.
DE Human prostate expression marker cDNA 25170.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.2%; Score 32.2; DB 5; Length 1522;
Best Local Similarity 50.3%; Pred. No. 79;
RESULT 770
ID ABA16847 standard; DNA; 1860 BP.
DE Human nervous system related polynucleotide SEQ ID NO 9178.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.2%; Score 32.2; DB 5; Length 1860;
Best Local Similarity 47.3%; Pred. No. 86;
RESULT 771
ID ABA16846 standard; DNA; 1861 BP.
DE Human nervous system related polynucleotide SEQ ID NO 9177.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.2%; Score 32.2; DB 5; Length 1861;
Best Local Similarity 47.3%; Pred. No. 86;
RESULT 772
ID ADA53739 standard; cDNA; 2566 BP.
DE Human coding sequence, SEQ ID 1307.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 4.2%; Score 32.2; DB 10; Length 2566;
Best Local Similarity 47.3%; Pred. No. 1e+02;
RESULT 773
ID ADC30795 standard; cDNA; 2854 BP.
DE Human novel cDNA sequence, SEQ ID NO:877.
PN WO2003029271-A2.
PD 10-APR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 4.2%; Score 32.2; DB 10; Length 2854;
Best Local Similarity 47.3%; Pred. No. 1.1e+02;
RESULT 774
ID ABL33642 standard; DNA; 6319 BP.
DE Human immune system associated gene SEQ ID NO: 1615.

PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.2%; Score 32.2; DB 6; Length 6319;
Best Local Similarity 52.5%; Pred. No. 1.5e+02;
RESULT 775
ID ABT03059 standard; DNA; 8904 BP.
DE Human breast specific coding sequence SEQ ID NO: 64.
PN WO200240672-A2.
PD 23-MAY-2002.
PA (DIAD-) DIADEXUS INC.
Query Match 4.2%; Score 32.2; DB 6; Length 8904;
Best Local Similarity 54.7%; Pred. No. 1.8e+02;
RESULT 776
ID ABT07637 standard; cDNA; 8905 BP.
DE Human breast cancer associated coding sequence SEQ ID NO: 116.
PN WO200264611-A1.
PD 22-AUG-2002.
PA (DIAD-) DIADEXUS INC.
Query Match 4.2%; Score 32.2; DB 6; Length 8905;
Best Local Similarity 54.7%; Pred. No. 1.8e+02;
RESULT 777
ID ADI72402 standard; DNA; 356 BP.
DE Human ovarian cancer DNA marker #5144.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.2%; Score 32; DB 5; Length 356;
Best Local Similarity 38.5%; Pred. No. 46;
RESULT 778
ID ADL37545 standard; DNA; 356 BP.
DE Human ovarian cancer DNA marker #11435.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.2%; Score 32; DB 5; Length 356;
Best Local Similarity 38.5%; Pred. No. 46;
RESULT 779
ID ACA46310 standard; DNA; 1026 BP.
DE Prokaryotic essential gene #27967.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.2%; Score 32; DB 8; Length 1026;
Best Local Similarity 50.7%; Pred. No. 75;
RESULT 780
ID AAS54908 standard; DNA; 1065 BP.
DE Staphylococcus aureus DNA for cellular proliferation protein #1220.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.2%; Score 32; DB 4; Length 1065;
Best Local Similarity 50.7%; Pred. No. 76;
RESULT 781
ID ACAS2696 standard; DNA; 2130 BP.
DE Prokaryotic essential gene #34353.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.2%; Score 32; DB 8; Length 2130;
Best Local Similarity 47.9%; Pred. No. 1.1e+02;
RESULT 782
ID ADJ40496 standard; cDNA; 4536 BP.
DE Plant cDNA #1496.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBOOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.

PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RIQUE D.
PA (ZHUT/) ZHU T.
Query Match 4.2%; Score 32; DB 12; Length 4536;
Best Local Similarity 58.3%; Pred. No. 1.5e+02;
RESULT 783
ID AAQ55753 standard; DNA; 4954 BP.
DE Escherichia coli genomic probe EC-34.
PN WO9401593-A1.
PD 20-JAN-1994.
PA (FUSO) FUSO PHARM IND LTD.
Query Match 4.2%; Score 32; DB 2; Length 4954;
Best Local Similarity 62.5%; Pred. No. 1.6e+02;
RESULT 784
ID ABZ77361 standard; DNA; 4954 BP.
DE Nucleotide sequence designated EC-34.
PN WO2002101037-A1.
PD 19-DEC-2002.
PA (FUSO) FUSO PHARM IND LTD.
Query Match 4.2%; Score 32; DB 8; Length 4954;
Best Local Similarity 62.5%; Pred. No. 1.6e+02;
RESULT 785
ID AAL51849 standard; DNA; 4954 BP.
DE Escherichia coli microbe identification-related DNA sequence #2.
PN WO200299133-A1.
PD 12-DEC-2002.
PA (FUSO) FUSO PHARM IND LTD.
PA (OHNO/) OHNO T.
Query Match 4.2%; Score 32; DB 10; Length 4954;
Best Local Similarity 62.5%; Pred. No. 1.6e+02;
RESULT 786
ID ABL32880 standard; DNA; 10197 BP.
DE Human immune system associated gene SEQ ID NO: 853.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.2%; Score 32; DB 6; Length 10197;
Best Local Similarity 47.9%; Pred. No. 2.2e+02;
RESULT 787
ID ABL92285 standard; DNA; 11015 BP.
DE Chemically treated DNA repair gene fragment complementary to #47.
PN WO200181622-A2.
PD 01-NOV-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.2%; Score 32; DB 6; Length 11015;
Best Local Similarity 51.4%; Pred. No. 2.3e+02;
RESULT 788
ID ABL49356 standard; DNA; 11015 BP.
DE Human polynucleotide associated with DNA replication SEQ ID NO 56.
PN WO200177377-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.2%; Score 32; DB 6; Length 11015;
Best Local Similarity 51.4%; Pred. No. 2.3e+02;
RESULT 789
ID AAD22336 standard; DNA; 11015 BP.
DE Chemically treated human genomic DNA #26 associated with DNA adducts.
PN WO200177378-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.2%; Score 32; DB 6; Length 11015;
Best Local Similarity 51.4%; Pred. No. 2.3e+02;
RESULT 790
ID ABL21130 standard; DNA; 19385 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 14863.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.2%; Score 32; DB 4; Length 19385;
Best Local Similarity 62.5%; Pred. No. 3e+02;
RESULT 791
ID ABV02994 standard; cDNA; 431 BP.

DE Human prostate expression marker cDNA 2985.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.2%; Score 31.8; DB 5; Length 431;
Best Local Similarity 52.8%; Pred. No. 58;
RESULT 792
ID AAH06229 standard; cDNA; 693 BP.
DE Human cDNA clone (5'-primer) SEQ ID NO:3064.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 4.2%; Score 31.8; DB 4; Length 693;
Best Local Similarity 56.1%; Pred. No. 72;
RESULT 793
ID AAK56975 standard; cDNA; 860 BP.
DE Human immune/haematopoietic antigen encoding cDNA SEQ ID NO:2035.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.2%; Score 31.8; DB 4; Length 860;
Best Local Similarity 49.7%; Pred. No. 80;
RESULT 794
ID ADL12361 standard; cDNA; 894 BP.
DE Human steroid-induced C3A liver cell cDNA #90.
PN US6673549-B1.
PD 06-JAN-2004.
PA (INCY-) INCYTE CORP.
Query Match 4.2%; Score 31.8; DB 12; Length 894;
Best Local Similarity 48.1%; Pred. No. 81;
RESULT 795
ID ADI41892 standard; DNA; 1316 BP.
DE Plant transcription factor polynucleotide #178.
PN US2004019927-A1.
PD 29-JAN-2004.
PA (SHER/) SHERMAN B K.
PA (RIEC/) RIECHMANN J L.
PA (JIAN/) JIANG C.
PA (HEAR/) HEARD J E.
PA (HAAK/) HAAKE V.
PA (CREE/) CREELMAN R A.
PA (RATC/) RATCLIFFE O.
PA (ADAM/) ADAM L J.
PA (REUB/) REUBER T L.
PA (KEDD/) KEDDIE J.
PA (BROU/) BROUN P E.
PA (PILG/) PILGRIM M L.
PA (DUBE/) DUBELL A N.
PA (PINE/) PINEDA O.
PA (YUGG/) YU G.
Query Match 4.2%; Score 31.8; DB 12; Length 1316;
Best Local Similarity 50.3%; Pred. No. 97;
RESULT 796
ID ADO61836 standard; DNA; 1316 BP.
DE Transcription factor G1863 coding sequence, SEQ ID 303.
PN WO2004031349-A2.
PD 15-APR-2004.
PA (MEND-) MENDEL BIOTECHNOLOGY INC.
Query Match 4.2%; Score 31.8; DB 12; Length 1316;
Best Local Similarity 50.3%; Pred. No. 97;
RESULT 797
ID ADO63008 standard; DNA; 1316 BP.
DE Transcription factor G1863 coding sequence, SEQ ID 1475.
PN WO2004031349-A2.
PD 15-APR-2004.
PA (MEND-) MENDEL BIOTECHNOLOGY INC.
Query Match 4.2%; Score 31.8; DB 12; Length 1316;
Best Local Similarity 50.3%; Pred. No. 97;
RESULT 798
ID ADE37134 standard; cDNA; 1322 BP.
DE Plant yield related polynucleotide clone G1863.
PN WO2003014327-A2.
PD 20-FEB-2003.

PA (MEND-) MENDEL BIOTECHNOLOGY INC.
Query Match 4.2%; Score 31.8; DB 10; Length 1322;
Best Local Similarity 50.3%; Pred. No. 97;
RESULT 799
ID AAZ93098 standard; DNA; 1438 BP.
DE Thiosulphate sulphurtransferase gene of wheat.
PN WO200006756-A1.
PD 10-FEB-2000.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 4.2%; Score 31.8; DB 3; Length 1438;
Best Local Similarity 57.6%; Pred. No. 1e+02;
RESULT 800
ID AAI60317 standard; cDNA; 4562 BP.
DE Human polynucleotide SEQ ID NO 4306.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.2%; Score 31.8; DB 4; Length 4562;
Best Local Similarity 56.1%; Pred. No. 1.7e+02;
RESULT 801
ID ABA18924 standard; DNA; 6554 BP.
DE Human nervous system related polynucleotide SEQ ID NO 11255.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.2%; Score 31.8; DB 5; Length 6554;
Best Local Similarity 49.1%; Pred. No. 2.1e+02;
RESULT 802
ID ABA18544 standard; DNA; 6554 BP.
DE Human nervous system related polynucleotide SEQ ID NO 10875.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.2%; Score 31.8; DB 5; Length 6554;
Best Local Similarity 49.1%; Pred. No. 2.1e+02;
RESULT 803
ID ABA18923 standard; DNA; 6567 BP.
DE Human nervous system related polynucleotide SEQ ID NO 11254.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.2%; Score 31.8; DB 5; Length 6567;
Best Local Similarity 49.1%; Pred. No. 2.1e+02;
RESULT 804
ID ABK31228 standard; DNA; 7234 BP.
DE Signal transduction associated gene modified DNA #36.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.2%; Score 31.8; DB 6; Length 7234;
Best Local Similarity 48.6%; Pred. No. 2.2e+02;
RESULT 805
ID ABK40017 standard; DNA; 18133 BP.
DE Human chemically pretreated gene sequence #50 strand 1.
PN WO200202806-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.2%; Score 31.8; DB 6; Length 18133;
Best Local Similarity 49.1%; Pred. No. 3.3e+02;
RESULT 806
ID ABL32940 standard; DNA; 18133 BP.
DE Human immune system associated gene SEQ ID NO: 913.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.2%; Score 31.8; DB 6; Length 18133;
Best Local Similarity 49.1%; Pred. No. 3.3e+02;
RESULT 807
ID ABA19669 standard; DNA; 32247 BP.
DE Human nervous system related polynucleotide SEQ ID NO 12000.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 4.2%; Score 31.8; DB 5; Length 32247;
Best Local Similarity 51.0%; Pred. No. 4.3e+02;
RESULT 808
Query Match 4.2%; Score 31.8; DB 6; Length 110000;
Best Local Similarity 46.6%; Pred. No. 7.6e+02;
RESULT 809
ID ADO79173 standard; DNA; 447894 BP.
DE KLF12 gene and surrounding region, SEQ ID 1.
Query Match 4.2%; Score 31.8; DB 12; Length 110000;
Best Local Similarity 48.1%; Pred. No. 7.6e+02;
RESULT 810
ID ABQ88207 standard; cDNA; 172570 BP.
DE Human osteoblast differentiation related cDNA SEQ ID NO 114.
PN WO200250301-A2.
PD 27-JUN-2002.
PA (GENE-) GENE LOGIC INC.
PA (PROC) PROCTER & GAMBLE CO.
Query Match 4.2%; Score 31.8; DB 6; Length 172570;
Best Local Similarity 56.1%; Pred. No. 9.4e+02;
RESULT 811
ID ADG99379 standard; DNA; 145 BP.
DE Kidney disease-associated gene-related mouse DNA sequence SeqID509.
PN WO2003091427-A1.
PD 06-NOV-2003.
PA (KANS-) KANSAS TECHNOLOGY LICENSING ORG CO LTD.
Query Match 4.1%; Score 31.6; DB 12; Length 145;
Best Local Similarity 56.9%; Pred. No. 40;
RESULT 812
ID AAK74840 standard; DNA; 424 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:29652.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.1%; Score 31.6; DB 4; Length 424;
Best Local Similarity 52.2%; Pred. No. 66;
RESULT 813
ID AAK74841 standard; DNA; 424 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:29653.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.1%; Score 31.6; DB 4; Length 424;
Best Local Similarity 52.2%; Pred. No. 66;
RESULT 814
ID AB254280 standard; cDNA; 541 BP.
DE Aspergillus oryzae polynucleotide SEQ ID NO 3393.
PN WO200279476-A1.
PD 10-OCT-2002.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (NARE-) NAT RES INST BREWING.
PA (NORQ) NAT FOOD RES INST MIN AGRIC.
Query Match 4.1%; Score 31.6; DB 8; Length 541;
Best Local Similarity 60.5%; Pred. No. 74;
RESULT 815
ID AAX04323 standard; DNA; 632 BP.
DE Human secreted protein gene 13 clone HSABI42.
PN WO9856804-A1.
PD 17-DEC-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.1%; Score 31.6; DB 2; Length 632;
Best Local Similarity 55.5%; Pred. No. 79;
RESULT 816
ID ADA15611 standard; DNA; 1500 BP.
DE A. thaliana recombinant polynucleotide, SEQ ID NO:166.
PN US2003061637-A1.
PD 27-MAR-2003.
PA (JIAN/) JIANG C.
PA (BROU/) BROUN P.
PA (RIEC/) RIECHMANN J L.
PA (PINE/) PINEDA O.
PA (ZHAN/) ZHANG J.
PA (YUGG/) YU G.
PA (PILG/) PILGRIM M.

PA (KEDD/) KEDDIE J.
PA (HEAR/) HEARD J.
PA (REUB/) REUBER L.
PA (RATC/) RATCLIFFE O.
PA (ADAM/) ADAM L.
PA (SAMA/) SAMAHA R.
Query Match 4.1%; Score 31.6; DB 9; Length 1500;
Best Local Similarity 48.9%; Pred. No. 1.2e+02;
RESULT 817
ID ABL21672 standard; DNA; 2216 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 16489.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.1%; Score 31.6; DB 4; Length 2216;
Best Local Similarity 58.5%; Pred. No. 1.4e+02;
RESULT 818
ID ADQ22935 standard; DNA; 2288 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5755.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 4.1%; Score 31.6; DB 12; Length 2288;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
RESULT 819
ID ABL33135 standard; DNA; 5252 BP.
DE Human immune system associated gene SEQ ID NO: 1108.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.1%; Score 31.6; DB 6; Length 5252;
Best Local Similarity 51.4%; Pred. No. 2.1e+02;
RESULT 820
ID ABK31398 standard; DNA; 5468 BP.
DE Signal transduction associated gene modified DNA #121.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.1%; Score 31.6; DB 6; Length 5468;
Best Local Similarity 51.4%; Pred. No. 2.2e+02;
RESULT 821
ID ABL70363 standard; DNA; 5468 BP.
DE Chemically treated cell signalling DNA sequence#127.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.1%; Score 31.6; DB 6; Length 5468;
Best Local Similarity 51.4%; Pred. No. 2.2e+02;
RESULT 822
ID AAS46583 standard; DNA; 6167 BP.
DE Tumour suppressor gene derived chemically modified sequence #305.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.1%; Score 31.6; DB 4; Length 6167;
Best Local Similarity 50.0%; Pred. No. 2.3e+02;
RESULT 823
ID ABL33838 standard; DNA; 6167 BP.
DE Human immune system associated gene SEQ ID NO: 1811.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.1%; Score 31.6; DB 6; Length 6167;
Best Local Similarity 50.0%; Pred. No. 2.3e+02;
RESULT 824
ID ABK31376 standard; DNA; 7037 BP.
DE Signal transduction associated gene modified DNA #110.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.1%; Score 31.6; DB 6; Length 7037;
Best Local Similarity 47.9%; Pred. No. 2.4e+02;
RESULT 825

ID AAD50032 standard; DNA; 9528 BP.
DE Human novel CpG-associated gene 1 (NCAG1) brain-expressed gene #1.
PN WO2002101044-A2.
PD 19-DEC-2002.
PA (JANC) JANSSEN PHARM NV.
Query Match 4.1%; Score 31.6; DB 10; Length 9528;
Best Local Similarity 46.1%; Pred. No. 2.8e+02;
RESULT 826
ID ABL34206 standard; DNA; 12601 BP.
DE Human immune system associated gene SEQ ID NO: 2179.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIC-) EPIGENOMICS AG.
Query Match 4.1%; Score 31.6; DB 6; Length 12601;
Best Local Similarity 49.5%; Pred. No. 3.2e+02;
RESULT 827
ID ABL32673 standard; DNA; 16287 BP.
DE Human immune system associated gene SEQ ID NO: 646.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIC-) EPIGENOMICS AG.
Query Match 4.1%; Score 31.6; DB 6; Length 16287;
Best Local Similarity 51.4%; Pred. No. 3.6e+02;
RESULT 828
ID AAD02701 standard; DNA; 27150 BP.
DE Human glycosyl sulfotransferase-6 (GST-6) genomic DNA #1.
PN WO200106015-A1.
PD 25-JAN-2001.
PA (REGC) UNIV CALIFORNIA.
Query Match 4.1%; Score 31.6; DB 4; Length 27150;
Best Local Similarity 46.1%; Pred. No. 4.6e+02;
RESULT 829
ID ABL10478 standard; cDNA; 29046 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 25916.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.1%; Score 31.6; DB 4; Length 29046;
Best Local Similarity 50.0%; Pred. No. 4.8e+02;
RESULT 830
Query Match 4.1%; Score 31.6; DB 10; Length 110000;
Best Local Similarity 47.1%; Pred. No. 8.8e+02;
RESULT 831
ID ACH36149 standard; cDNA; 375 BP.
DE Human endothelial cell cDNA #4282.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 4.1%; Score 31.4; DB 9; Length 375;
Best Local Similarity 71.9%; Pred. No. 71;
RESULT 832
ID ABL81191 standard; cDNA; 441 BP.
DE Human ovarian cancer related cDNA clone SEQ ID NO:4169.
PN WO200192581-A2.
PD 06-DEC-2001.
PA (CORI-) CORIXA CORP.
Query Match 4.1%; Score 31.4; DB 6; Length 441;
Best Local Similarity 50.3%; Pred. No. 77;
RESULT 833
ID AAF64742 standard; cDNA; 451 BP.
DE Novel human polynucleotide, SEQ ID NO: 498.
PN WO200102568-A2.
PD 11-JAN-2001.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 4.1%; Score 31.4; DB 5; Length 451;
Best Local Similarity 56.2%; Pred. No. 78;
RESULT 834
ID ABT41119 standard; DNA; 452 BP.

DE Toxicity modelling related rat gene SEQ ID No 821.
PN WO200295000-A2.
PD 28-NOV-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 4.1%; Score 31.4; DB 10; Length 452;
Best Local Similarity 54.9%; Pred. No. 78;
RESULT 835
ID ADP72083 standard; DNA; 452 BP.
DE Renal toxin progression gene marker #672.
PN WO2004048598-A2.
PD 10-JUN-2004.
PA (GENE-) GENE LOGIC INC.
Query Match 4.1%; Score 31.4; DB 12; Length 452;
Best Local Similarity 54.9%; Pred. No. 78;
RESULT 836
ID ADD46193 standard; DNA; 603 BP.
DE Human gene BG203058, SEQ ID NO 11868.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 4.1%; Score 31.4; DB 10; Length 603;
Best Local Similarity 47.7%; Pred. No. 89;
RESULT 837
ID AAT67376 standard; DNA; 864 BP.
DE H. pylori cell envelope transporter protein ORF 13726562.aa.
PN WO9640893-A1.
PD 19-DEC-1996.
PA (ASTR) ASTRA AB.
Query Match 4.1%; Score 31.4; DB 2; Length 864;
Best Local Similarity 51.8%; Pred. No. 1.1e+02;
RESULT 838
ID AAT67872 standard; DNA; 1131 BP.
DE H. pylori transporter protein ORF 02aell61loxf11.
PN WO9640893-A1.
PD 19-DEC-1996.
PA (ASTR) ASTRA AB.
Query Match 4.1%; Score 31.4; DB 2; Length 1131;
Best Local Similarity 51.8%; Pred. No. 1.2e+02;
RESULT 839
ID AAC79710 standard; cDNA; 1274 BP.
DE Human secreted protein gene 30 SEQ ID NO:40.
PN WO200058339-A2.
PD 05-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.1%; Score 31.4; DB 3; Length 1274;
Best Local Similarity 50.3%; Pred. No. 1.3e+02;
RESULT 840
ID AAV59612 standard; DNA; 1313 BP.
DE Human secreted protein gene 102 clone HE2BG03.
PN WO9839448-A2.
PD 11-SEP-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.1%; Score 31.4; DB 2; Length 1313;
Best Local Similarity 47.3%; Pred. No. 1.3e+02;
RESULT 841
ID ABS73599 standard; cDNA; 1313 BP.
DE Human cDNA #1 for novel secreted protein gene 102.
PN US6420526-B1.
PD 16-JUL-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.1%; Score 31.4; DB 6; Length 1313;
Best Local Similarity 47.3%; Pred. No. 1.3e+02;
RESULT 842
ID ACD82742 standard; cDNA; 1313 BP.
DE cDNA sequence #102 containing coding region of a human secreted protein.
PN US2003049618-A1.
PD 13-MAR-2003.
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (SOPP/) SOPPET D R.
PA (CART/) CARTER K C.
PA (BEDN/) BEDNARIK D P.

PA (ENDR/) ENDRESS G A.
PA (YUGG/) YU G.
PA (NIJJ/) NI J.
PA (FENG/) FENG P.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (DUAN/) DUAN D R.
PA (HUJJ/) HU J.
PA (FLOR/) FLORENCE K A.
PA (OLSE/) OLSEN H S.
PA (FISC/) FISCHER C L.
PA (EBNE/) EBNER R.
PA (BREW/) BREWER L A.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (LAF/) LAFLEUR D W.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
Query Match
Best Local Similarity 4.1%; Score 31.4; DB 9; Length 1313;
47.3%; Pred. No. 1.3e+02;
RESULT 843
ID ADI22827 standard; cDNA; 1313 BP.
DE cDNA encoding novel human secreted protein seq id 112.
PN US2003175858-A1.
PD 18-SEP-2003.
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (SOPP/) SOPPET D R.
PA (CART/) CARTER K C.
PA (BEDN/) BEDNARIK D P.
PA (ENDR/) ENDRESS G A.
PA (YUGG/) YU G.
PA (NIJJ/) NI J.
PA (FENG/) FENG P.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (DUAN/) DUAN D R.
PA (HUJJ/) HU J.
PA (FLOR/) FLORENCE K A.
PA (OLSE/) OLSEN H S.
PA (FISC/) FISCHER C L.
PA (EBNE/) EBNER R.
PA (BREW/) BREWER L A.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (LAF/) LAFLEUR D W.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
Query Match
Best Local Similarity 4.1%; Score 31.4; DB 10; Length 1313;
47.3%; Pred. No. 1.3e+02;
RESULT 844
ID ADH73829 standard; cDNA; 1313 BP.
DE Human secreted protein cDNA #102.
PN US2003225248-A1.
PD 04-DEC-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 4.1%; Score 31.4; DB 12; Length 1313;
47.3%; Pred. No. 1.3e+02;
RESULT 845
ID AAF32735 standard; cDNA; 1893 BP.
DE Human secreted protein gene 37 SEQ ID NO:47.
PN WO200077255-A1.
PD 21-DEC-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 4.1%; Score 31.4; DB 4; Length 1893;
56.2%; Pred. No. 1.5e+02;
RESULT 846
ID ACA47527 standard; DNA; 1896 BP.
DE Prokaryotic essential gene #29184.

PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 4.1%; Score 31.4; DB 8; Length 1896;
48.1%; Pred. No. 1.5e+02;
RESULT 847
ID AAV59644 standard; DNA; 1944 BP.
DE Human secreted protein gene 134 clone HPMGD24.
PN WO9839448-A2.
PD 11-SEP-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 4.1%; Score 31.4; DB 2; Length 1944;
71.9%; Pred. No. 1.5e+02;
RESULT 848
ID ABS73631 standard; cDNA; 1944 BP.
DE Human cDNA #1 for novel secreted protein gene 134.
PN US6420526-B1.
PD 16-JUL-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 4.1%; Score 31.4; DB 6; Length 1944;
71.9%; Pred. No. 1.5e+02;
RESULT 849
ID ACD82774 standard; cDNA; 1944 BP.
DE cDNA sequence #134 containing coding region of a human secreted protein.
PN US2003049618-A1.
PD 13-MAR-2003.
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (SOPP/) SOPPET D R.
PA (CART/) CARTER K C.
PA (BEDN/) BEDNARIK D P.
PA (ENDR/) ENDRESS G A.
PA (YUGG/) YU G.
PA (NIJJ/) NI J.
PA (FENG/) FENG P.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (DUAN/) DUAN D R.
PA (HUJJ/) HU J.
PA (FLOR/) FLORENCE K A.
PA (OLSE/) OLSEN H S.
PA (FISC/) FISCHER C L.
PA (EBNE/) EBNER R.
PA (BREW/) BREWER L A.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (LAF/) LAFLEUR D W.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
Query Match
Best Local Similarity 4.1%; Score 31.4; DB 9; Length 1944;
71.9%; Pred. No. 1.5e+02;
RESULT 850
ID ADI22859 standard; cDNA; 1944 BP.
DE cDNA encoding novel human secreted protein seq id 144.
PN US2003175858-A1.
PD 18-SEP-2003.
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (SOPP/) SOPPET D R.
PA (CART/) CARTER K C.
PA (BEDN/) BEDNARIK D P.
PA (ENDR/) ENDRESS G A.
PA (YUGG/) YU G.
PA (NIJJ/) NI J.
PA (FENG/) FENG P.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (DUAN/) DUAN D R.
PA (HUJJ/) HU J.
PA (FLOR/) FLORENCE K A.

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PA (OLSE/) OLSEN H S.
PA (FISC/) FISCHER C L.
PA (EBNE/) EBNER R.
PA (BREW/) BREWER L A.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (LAFL/) LAFLEUR D W.
PA (LIVY/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
Query Match
Best Local Similarity 4.1%; Score 31.4; DB 10; Length 1944;
RESULT 851
ID ADH73861 standard; cDNA; 1944 BP.
DE Human secreted protein cDNA #134.
PN US2003225248-A1.
PD 04-DEC-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 4.1%; Score 31.4; DB 12; Length 1944;
RESULT 852
ID AAC36715 standard; DNA; 1993 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 14818.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 4.1%; Score 31.4; DB 3; Length 1993;
RESULT 853
ID AAF26568 standard; DNA; 2108 BP.
DE DNA encoding human secreted protein #22.
PN WO200076531-A1.
PD 21-DEC-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 4.1%; Score 31.4; DB 4; Length 2108;
RESULT 854
ID AAF45111 standard; cDNA; 2266 BP.
DE Human secreted protein coding sequence SEQ ID NO: 50.
PN WO200077023-A1.
PD 21-DEC-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 4.1%; Score 31.4; DB 4; Length 2266;
RESULT 855
ID AAS23423 standard; DNA; 2307 BP.
DE Candida albicans essential gene CAYMR277W (FCP1).
PN WO200160975-A2.
PD 23-AUG-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 4.1%; Score 31.4; DB 4; Length 2307;
RESULT 856
ID ABZ31771 standard; DNA; 2307 BP.
DE Candida albicans essential gene SEQ ID NO 6058.
PN WO200253728-A2.
PD 11-JUL-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 4.1%; Score 31.4; DB 6; Length 2307;
RESULT 857
ID ABL25870 standard; DNA; 2333 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 29083.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Query Match
Best Local Similarity 4.1%; Score 31.4; DB 4; Length 2333;
RESULT 858
ID AAH15891 standard; cDNA; 2349 BP.
DE Human cDNA sequence SEQ ID NO:14430.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match
Best Local Similarity 4.1%; Score 31.4; DB 4; Length 2349;
RESULT 859
ID AAH77802 standard; DNA; 2349 BP.
DE Nucleotide sequence of a human liver-associated gene.
PN WO200109318-A1.
PD 08-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match
Best Local Similarity 4.1%; Score 31.4; DB 4; Length 2349;
RESULT 860
ID ABL27076 standard; DNA; 2879 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 32701.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Query Match
Best Local Similarity 4.1%; Score 31.4; DB 4; Length 2879;
RESULT 861
ID AAC75938 standard; cDNA; 4547 BP.
DE Human ORF1493 polynucleotide sequence SEQ ID NO:2985.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 4.1%; Score 31.4; DB 3; Length 4547;
RESULT 862
ID AAI58531 standard; cDNA; 4562 BP.
DE Human polynucleotide SEQ ID NO 734.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 4.1%; Score 31.4; DB 4; Length 4562;
RESULT 863
ID ADQ98748 standard; cDNA; 4562 BP.
DE DNA encoding human GPCR-like protein seqid 418.
PN US6569662-B1.
PD 27-MAY-2003.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 4.1%; Score 31.4; DB 5; Length 4562;
RESULT 864
ID ADB48508 standard; cDNA; 4562 BP.
DE Novel human cDNA SEQ ID NO 418.
PN US2003104529-A1.
PD 05-JUN-2003.
PA (ZHOU/) ZHOU P.
PA (TANG/) TANG Y T.
PA (LIUC/) LIU C.
PA (ASUN/) ASUNDI V.
PA (DRMA/) DRMANAC R T.
Query Match
Best Local Similarity 4.1%; Score 31.4; DB 9; Length 4562;
RESULT 865
ID AAK52963 standard; cDNA; 4563 BP.
DE Human polynucleotide SEQ ID NO 2492.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 4.1%; Score 31.4; DB 4; Length 4563;
RESULT 866
ID ADQ20329 standard; DNA; 4563 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 3149.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match
Best Local Similarity 4.1%; Score 31.4; DB 12; Length 4563;
RESULT 867
ID AAK51979 standard; cDNA; 4567 BP.
DE Human polynucleotide SEQ ID NO 524.
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PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.1%; Score 31.4; DB 4; Length 4567;
Best Local Similarity 56.2%; Pred. No. 2.3e+02;
RESULT 868
ID AAH24065 standard; DNA; 4590 BP.
DE Yeast AOD9604-associated DNA sequence, SEQ ID NO:1.
PN WO200133977-A1.
PD 17-MAY-2001.
PA (META-) METABOLIC PHARM LTD.
Query Match 4.1%; Score 31.4; DB 5; Length 4590;
Best Local Similarity 14.8%; Pred. No. 2.3e+02;
RESULT 869
ID ADL61925 standard; DNA; 4689 BP.
DE Human ovarian cancer DNA marker #20137.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.1%; Score 31.4; DB 5; Length 4689;
Best Local Similarity 56.2%; Pred. No. 2.3e+02;
RESULT 870
ID ADQ24340 standard; DNA; 4696 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7160.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 4.1%; Score 31.4; DB 12; Length 4696;
Best Local Similarity 56.2%; Pred. No. 2.3e+02;
RESULT 871
ID ABQ76258 standard; DNA; 4699 BP.
DE Human 7B6 DNA.
PN WO200264777-A2.
PD 22-AUG-2002.
PA (BADI) BASF-LYNX BIOSCIENCE AG.
Query Match 4.1%; Score 31.4; DB 6; Length 4699;
Best Local Similarity 56.2%; Pred. No. 2.3e+02;
RESULT 872
ID ABL33916 standard; DNA; 5464 BP.
DE Human immune system associated gene SEQ ID NO: 1889.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.1%; Score 31.4; DB 6; Length 5464;
Best Local Similarity 54.9%; Pred. No. 2.5e+02;
RESULT 873
ID ABK31452 standard; DNA; 5464 BP.
DE Signal transduction associated gene modified DNA #148.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.1%; Score 31.4; DB 6; Length 5464;
Best Local Similarity 54.9%; Pred. No. 2.5e+02;
RESULT 874
ID ABL70429 standard; DNA; 5464 BP.
DE Chemically treated cell signalling DNA sequence#160.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.1%; Score 31.4; DB 6; Length 5464;
Best Local Similarity 54.9%; Pred. No. 2.5e+02;
RESULT 875
ID AAS63340 standard; DNA; 6207 BP.
DE Chemically pretreated metabolism associated gene #35.
PN WO200176451-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.1%; Score 31.4; DB 6; Length 6207;
Best Local Similarity 51.8%; Pred. No. 2.7e+02;
RESULT 876
ID AAK89991 standard; DNA; 12244 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 3567.
PN WO200155314-A2.

PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.1%; Score 31.4; DB 4; Length 12244;
Best Local Similarity 64.4%; Pred. No. 3.6e+02;
RESULT 877
ID ABL70575 standard; DNA; 19576 BP.
DE Chemically treated cell signalling DNA sequence#233.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.1%; Score 31.4; DB 6; Length 19576;
Best Local Similarity 47.3%; Pred. No. 4.5e+02;
RESULT 878
ID AAS61258 standard; DNA; 19576 BP.
DE Human gene regulation-associated gene oligonucleotide #213.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.1%; Score 31.4; DB 6; Length 19576;
Best Local Similarity 47.3%; Pred. No. 4.5e+02;
RESULT 879
ID AAK77120 standard; DNA; 22977 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:31932.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.1%; Score 31.4; DB 4; Length 22977;
Best Local Similarity 57.7%; Pred. No. 4.9e+02;
RESULT 880
ID AAF27996 standard; DNA; 48000 BP.
DE Human calcium sensitive potassium channel beta3 subunits coding sequence.
PN WO200105828-A1.
PD 25-JAN-2001.
PA (MERI) MERCK & CO INC.
Query Match 4.1%; Score 31.4; DB 4; Length 48000;
Best Local Similarity 46.5%; Pred. No. 6.9e+02;
RESULT 881
ID ABL70575 standard; DNA; 19576 BP.
DE Chemically treated cell signalling DNA sequence#233.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.1%; Score 31.4; DB 6; Length 19576;
Best Local Similarity 47.3%; Pred. No. 4.5e+02;
RESULT 882
ID ADQ19901 standard; DNA; 158811 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2720.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 4.1%; Score 31.4; DB 12; Length 158811;
Best Local Similarity 46.9%; Pred. No. 1.2e+03;
RESULT 883
ID ADC24763 standard; DNA; 334462 BP.
DE Human wild type HNL4X genomic sequence.
PN WO2003045998-A2.
PD 05-JUN-2003.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (INSP) INST PASTEUR.
PA (ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.
Query Match 4.1%; Score 31.4; DB 10; Length 334462;
Best Local Similarity 64.4%; Pred. No. 1.6e+03;
RESULT 884
ID ABV49114 standard; cDNA; 319 BP.
DE Human prostate expression marker cDNA 49105.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.1%; Score 31.2; DB 5; Length 319;
Best Local Similarity 60.7%; Pred. No. 76;
RESULT 885
ID ABV19340 standard; cDNA; 387 BP.
DE Human prostate expression marker cDNA 19331.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.1%; Score 31.2; DB 5; Length 387;
Best Local Similarity 60.7%; Pred. No. 83;

RESULT 886
ID ACH48040 standard; cDNA; 452 BP.
DE Human lung tumour cDNA #173.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 4.1%; Score 31.2; DB 9; Length 452;
Best Local Similarity 58.7%; Pred. No. 90;
RESULT 887
ID ABV94430 standard; cDNA; 520 BP.
DE Breast carcinoma related nucleotide sequence SEQ ID NO:421.
PN WO200246467-A2.
PD 13-JUN-2002.
PA (IPSO-) IPSOGEN.
Query Match 4.1%; Score 31.2; DB 6; Length 520;
Best Local Similarity 58.7%; Pred. No. 96;
RESULT 888
ID ADF79804 standard; DNA; 532 BP.
DE Leukaemia-related DNA sequence #360.
PN WO2003039443-A2.
PD 15-MAY-2003.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA (UYLU-) UNIV LUDWIG MAXIMILIANS.
PA (HAPE/) HAPERLACH T.
PA (SCHO/) SCHOCH C.
PA (KERN/) KERN W.
Query Match 4.1%; Score 31.2; DB 10; Length 532;
Best Local Similarity 58.7%; Pred. No. 97;
RESULT 889
ID ABS73206 standard; DNA; 747 BP.
DE Human translocation (4; 11)(q21; q23) #1.
PN WO200269900-A2.
PD 12-SEP-2002.
PA (CONF-) CONFORMA THERAPEUTICS CORP.
Query Match 4.1%; Score 31.2; DB 6; Length 747;
Best Local Similarity 57.0%; Pred. No. 1.1e+02;
RESULT 890
ID AAA98305 standard; DNA; 982 BP.
DE Human MSH6 fragment 8/exon 8 to 10 DNA.
PN DE19909878-A1.
PD 07-SEP-2000.
PA (UYDR) UNIV DRESDEN TECH.
Query Match 4.1%; Score 31.2; DB 3; Length 982;
Best Local Similarity 66.2%; Pred. No. 1.3e+02;
RESULT 891
ID ACF72045 standard; DNA; 1146 BP.
DE Photorehabdus luminescens nucleotide sequence #10512.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 4.1%; Score 31.2; DB 10; Length 1146;
Best Local Similarity 50.7%; Pred. No. 1.4e+02;
RESULT 892
ID AAC50967 standard; DNA; 1232 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 66790.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.1%; Score 31.2; DB 3; Length 1232;
Best Local Similarity 49.1%; Pred. No. 1.4e+02;
RESULT 893
ID AAI68576 standard; DNA; 1355 BP.
DE L. esculentum SUT2 encoding DNA fragment.
PN WO200173086-A2.
PD 04-OCT-2001.
PA (FROM/) FROMMER W.
Query Match 4.1%; Score 31.2; DB 4; Length 1355;
Best Local Similarity 51.4%; Pred. No. 1.5e+02;
RESULT 894

ID ADA29148 standard; DNA; 1413 BP.
DE DNA encoding Acinetobacter baumannii protein #435.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.1%; Score 31.2; DB 9; Length 1413;
Best Local Similarity 57.0%; Pred. No. 1.5e+02;
RESULT 895
ID AAH50960 standard; cDNA; 1466 BP.
DE Plastidial delta 9 ACP desaturase partial clone nucleotide sequence.
PN WO200138484-A2.
PD 31-MAY-2001.
PA (BADI) BASF PLANT SCI GMBH.
Query Match 4.1%; Score 31.2; DB 5; Length 1466;
Best Local Similarity 60.7%; Pred. No. 1.6e+02;
RESULT 896
ID AAC50961 standard; DNA; 1731 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 66767.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.1%; Score 31.2; DB 3; Length 1731;
Best Local Similarity 49.1%; Pred. No. 1.7e+02;
RESULT 897
ID AAC44647 standard; DNA; 1735 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 43597.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.1%; Score 31.2; DB 3; Length 1735;
Best Local Similarity 49.1%; Pred. No. 1.7e+02;
RESULT 898
ID AAI68593 standard; DNA; 1818 BP.
DE S. tuberosum SUT2 encoding DNA.
PN WO200173086-A2.
PD 04-OCT-2001.
PA (FROM/) FROMMER W.
Query Match 4.1%; Score 31.2; DB 4; Length 1818;
Best Local Similarity 51.4%; Pred. No. 1.7e+02;
RESULT 899
ID ACF79843 standard; cDNA; 2621 BP.
DE Mouse anion exchanger SLC26A11 cDNA.
PN WO2003072756-A2.
PD 04-SEP-2003.
PA (UYVA-) UNIV VANDERBILT.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
PA (UYCA-) UNIV CASE WESTERN RESERVE.
Query Match 4.1%; Score 31.2; DB 10; Length 2621;
Best Local Similarity 55.6%; Pred. No. 2e+02;
RESULT 900
ID ADL83155 standard; cDNA; 3262 BP.
DE Human PRO84309 cDNA, SEQ ID 357.
PN WO2004024097-A2.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 31.2; DB 12; Length 3262;
Best Local Similarity 66.2%; Pred. No. 2.3e+02;
RESULT 901
ID ADO19324 standard; cDNA; 3262 BP.
DE Human PRO polynucleotide #128.
PN WO2004043361-A2.
PD 27-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 31.2; DB 12; Length 3262;
Best Local Similarity 66.2%; Pred. No. 2.3e+02;
RESULT 902
ID AAS73923 standard; cDNA; 3650 BP.
DE DNA encoding novel human diagnostic protein #9727.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.1%; Score 31.2; DB 5; Length 3650;
Best Local Similarity 52.3%; Pred. No. 2.4e+02;
RESULT 903
ID AAL06092 standard; DNA; 4800 BP.

DE Human reproductive system related antigen DNA SEQ ID NO: 8780.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.1%; Score 31.2; DB 4; Length 4800;
Best Local Similarity 55.6%; Pred. No. 2.7e+02;
RESULT 904
ID ABL98657 standard; DNA; 4800 BP.
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 3309.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.1%; Score 31.2; DB 4; Length 4800;
Best Local Similarity 55.6%; Pred. No. 2.7e+02;
RESULT 905
ID AAL06093 standard; DNA; 4845 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 8781.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.1%; Score 31.2; DB 4; Length 4845;
Best Local Similarity 55.6%; Pred. No. 2.7e+02;
RESULT 906
ID ABL98658 standard; DNA; 4845 BP.
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 3310.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.1%; Score 31.2; DB 4; Length 4845;
Best Local Similarity 55.6%; Pred. No. 2.7e+02;
RESULT 907
ID ABK31540 standard; DNA; 6045 BP.
DE Signal transduction associated gene modified DNA #192.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.1%; Score 31.2; DB 6; Length 6045;
Best Local Similarity 49.4%; Pred. No. 3e+02;
RESULT 908
ID ABL70623 standard; DNA; 6045 BP.
DE Chemically treated cell signalling DNA sequence#257.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.1%; Score 31.2; DB 6; Length 6045;
Best Local Similarity 49.4%; Pred. No. 3e+02;
RESULT 909
ID AAZ23433 standard; DNA; 6450 BP.
DE Human estrogen receptor DNA.
PN WO9945944-A1.
PD 16-SEP-1999.
PA (BURN-) BURNHAM INST.
Query Match 4.1%; Score 31.2; DB 2; Length 6450;
Best Local Similarity 58.7%; Pred. No. 3.1e+02;
RESULT 910
ID ABK89695 standard; DNA; 6450 BP.
DE Oestrogen receptor alpha nucleic acid comprising A908G mutation, #1.
PN WO200257283-A1.
PD 25-JUL-2002.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
Query Match 4.1%; Score 31.2; DB 6; Length 6450;
Best Local Similarity 58.7%; Pred. No. 3.1e+02;
RESULT 911
ID ABK89703 standard; DNA; 6450 BP.
DE Oestrogen receptor alpha nucleic acid comprising A908G mutation, #7.
PN WO200257283-A1.
PD 25-JUL-2002.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
Query Match 4.1%; Score 31.2; DB 6; Length 6450;
Best Local Similarity 58.7%; Pred. No. 3.1e+02;
RESULT 912
ID ABV94431 standard; cDNA; 6450 BP.
DE Breast carcinoma related nucleotide sequence SEQ ID NO:422.

PN WO200246467-A2.
PD 13-JUN-2002.
PA (IPSO-) IPSOGEN.
Query Match 4.1%; Score 31.2; DB 6; Length 6450;
Best Local Similarity 58.7%; Pred. No. 3.1e+02;
RESULT 913
ID ABZ23389 standard; cDNA; 6450 BP.
DE Reverse complement of human oestrogen receptor alpha cDNA.
PN WO200270699-A2.
PD 12-SEP-2002.
PA (LION-) LION BIOSCIENCE AG.
Query Match 4.1%; Score 31.2; DB 6; Length 6450;
Best Local Similarity 58.7%; Pred. No. 3.1e+02;
RESULT 914
ID ABZ23388 standard; cDNA; 6450 BP.
DE Nucleotide sequence of human oestrogen receptor alpha.
PN WO200270699-A2.
PD 12-SEP-2002.
PA (LION-) LION BIOSCIENCE AG.
Query Match 4.1%; Score 31.2; DB 6; Length 6450;
Best Local Similarity 58.7%; Pred. No. 3.1e+02;
RESULT 915
ID ABX12085 standard; cDNA; 6450 BP.
DE cDNA encoding a human oestrogen receptor.
PN US2002164581-A1.
PD 07-NOV-2002.
PA (CHAN/) CHANG C.
Query Match 4.1%; Score 31.2; DB 8; Length 6450;
Best Local Similarity 58.7%; Pred. No. 3.1e+02;
RESULT 916
ID ACC50140 standard; cDNA; 6450 BP.
DE Breast cancer associated cDNA sequence SEQ ID NO:127.
PN WO2003004989-A2.
PD 16-JAN-2003.
PA (MILL-) MILLENIUM PHARM INC.
Query Match 4.1%; Score 31.2; DB 8; Length 6450;
Best Local Similarity 58.7%; Pred. No. 3.1e+02;
RESULT 917
ID ABX93797 standard; cDNA; 6450 BP.
DE Human oestrogen receptor alpha (ER-alpha) cDNA.
PN US2002187495-A1.
PD 12-DEC-2002.
PA (HERR/) HERRINGTON D M.
PA (HOWA/) HOWARD T D.
PA (HAWK/) HAWKINS G A.
PA (MEYE/) MEYERS D A.
Query Match 4.1%; Score 31.2; DB 8; Length 6450;
Best Local Similarity 58.7%; Pred. No. 3.1e+02;
RESULT 918
ID ADB81383 standard; DNA; 6450 BP.
DE DNA sequence of the human oestrogen receptor alpha mRNA.
PN WO2003052072-A2.
PD 26-JUN-2003.
PA (ISIS-) ISIS PHARM INC.
Query Match 4.1%; Score 31.2; DB 10; Length 6450;
Best Local Similarity 58.7%; Pred. No. 3.1e+02;
RESULT 919
ID ADD25499 standard; DNA; 6450 BP.
DE Binding domain-immunoglobulin fusion protein-associated DNA #34.
PN US2003118592-A1.
PD 26-JUN-2003.
PA (GENE-) GENE-CRAFT INC.
Query Match 4.1%; Score 31.2; DB 10; Length 6450;
Best Local Similarity 58.7%; Pred. No. 3.1e+02;
RESULT 920
ID ADEi2135 standard; DNA; 6450 BP.
DE Human oestrogen receptor alpha DNA.
PN US2003199472-A1.
PD 23-OCT-2003.
PA (TEXA) UNIV TEXAS SYSTEM.
PA (NOUN) UNIV NORTHWESTERN.
Query Match 4.1%; Score 31.2; DB 10; Length 6450;
Best Local Similarity 58.7%; Pred. No. 3.1e+02;

RESULT 921
ID ADF76402 standard; cDNA; 6450 BP.
DE Novel human secreted and transmembrane protein cDNA SeqID 75.
PN WO2003072035-A2.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 4.1%; Score 31.2; DB 10; Length 6450;
Best Local Similarity 58.7%; Pred. No. 3.1e+02;
RESULT 922
ID ADG89355 standard; DNA; 6450 BP.
DE Cancer detection method related gene #18.
PN WO2003078662-A1.
PD 25-SEP-2003.
PA (GENO-) GENOMIC HEALTH INC.
Query Match 4.1%; Score 31.2; DB 10; Length 6450;
Best Local Similarity 58.7%; Pred. No. 3.1e+02;
RESULT 923
ID ADF83093 standard; DNA; 6450 BP.
DE Human testicular orphan nuclear receptor 4 (TR4) DNA.
PN WO2003100028-A2.
PD 04-DEC-2003.
PA (UYRP) UNIV ROCHESTER.
Query Match 4.1%; Score 31.2; DB 12; Length 6450;
Best Local Similarity 58.7%; Pred. No. 3.1e+02;
RESULT 924
ID ADF72329 standard; cDNA; 6450 BP.
DE Human androgen receptor nucleotide sequence SEQ ID NO:25.
PN WO2003103595-A2.
PD 18-DEC-2003.
PA (UYRP) UNIV ROCHESTER.
Query Match 4.1%; Score 31.2; DB 12; Length 6450;
Best Local Similarity 58.7%; Pred. No. 3.1e+02;
RESULT 925
ID ADP07306 standard; DNA; 6450 BP.
DE Human ESR1 DNA.
PN DE10255104-A1.
PD 11-MAR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.1%; Score 31.2; DB 12; Length 6450;
Best Local Similarity 58.7%; Pred. No. 3.1e+02;
RESULT 926
ID ADP05662 standard; DNA; 6450 BP.
DE Human nuclear receptor protein gene SeqID36.
PN WO2004045369-A2.
PD 03-JUN-2004.
PA (NURA-) NURA INC.
Query Match 4.1%; Score 31.2; DB 12; Length 6450;
Best Local Similarity 58.7%; Pred. No. 3.1e+02;
RESULT 927
ID ACC46160 standard; cDNA; 6468 BP.
DE Human dithp receptor-encoding cDNA.
PN WO200297031-A2.
PD 05-DEC-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 4.1%; Score 31.2; DB 8; Length 6468;
Best Local Similarity 58.7%; Pred. No. 3.1e+02;
RESULT 928
ID ADB81390 standard; DNA; 8566 BP.
DE Concatenated sequence of exons from chromosome 6 related to ESR-alpha.
PN WO2003052072-A2.
PD 26-JUN-2003.
PA (ISIS-) ISIS PHARM INC.
Query Match 4.1%; Score 31.2; DB 10; Length 8566;
Best Local Similarity 58.7%; Pred. No. 3.5e+02;
RESULT 929
ID ABL14994 standard; cDNA; 13843 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 39464.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.1%; Score 31.2; DB 4; Length 13843;
Best Local Similarity 52.3%; Pred. No. 4.4e+02;
RESULT 930
ID AAL04663 standard; DNA; 22073 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 7351.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.1%; Score 31.2; DB 4; Length 22073;
Best Local Similarity 58.7%; Pred. No. 5.5e+02;
RESULT 931
ID ABL97570 standard; DNA; 22073 BP.
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 2222.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.1%; Score 31.2; DB 4; Length 22073;
Best Local Similarity 58.7%; Pred. No. 5.5e+02;
RESULT 932
ID ABZ74560 standard; DNA; 22073 BP.
DE Secreted protein gene 351 genomic fragment HTXDB22, SEQ ID NO:1707.
PN WO200277013-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.1%; Score 31.2; DB 8; Length 22073;
Best Local Similarity 58.7%; Pred. No. 5.5e+02;
RESULT 933
ID ABZ68092 standard; DNA; 22073 BP.
DE Human secreted protein encoding genomic DNA SEQ ID NO 1615.
PN WO200277186-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.1%; Score 31.2; DB 10; Length 22073;
Best Local Similarity 58.7%; Pred. No. 5.5e+02;
RESULT 934
ID ABL09362 standard; cDNA; 24066 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 22568.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.1%; Score 31.2; DB 4; Length 24066;
Best Local Similarity 51.4%; Pred. No. 5.8e+02;
RESULT 935
Query Match 4.1%; Score 31.2; DB 6; Length 65237;
Best Local Similarity 58.7%; Pred. No. 9.1e+02;
RESULT 936
Query Match 4.1%; Score 31.2; DB 6; Length 65237;
Best Local Similarity 58.7%; Pred. No. 9.1e+02;
RESULT 937
Query Match 4.1%; Score 31.2; DB 8; Length 65237;
Best Local Similarity 58.7%; Pred. No. 9.1e+02;
RESULT 938
Query Match 4.1%; Score 31.2; DB 10; Length 92000;
Best Local Similarity 58.7%; Pred. No. 1.1e+03;
RESULT 939
Query Match 4.1%; Score 31.2; DB 4; Length 110000;
Best Local Similarity 47.9%; Pred. No. 1.2e+03;
RESULT 940
Query Match 4.1%; Score 31.2; DB 4; Length 110000;
Best Local Similarity 47.9%; Pred. No. 1.2e+03;
RESULT 941
Query Match 4.1%; Score 31.2; DB 6; Length 110000;
Best Local Similarity 47.9%; Pred. No. 1.2e+03;
RESULT 942
Query Match 4.1%; Score 31.2; DB 6; Length 110000;
Best Local Similarity 47.9%; Pred. No. 1.2e+03;
RESULT 943
Query Match 4.1%; Score 31.2; DB 10; Length 110000;
Best Local Similarity 50.7%; Pred. No. 1.2e+03;
RESULT 944
Query Match 4.1%; Score 31.2; DB 10; Length 110000;
Best Local Similarity 50.7%; Pred. No. 1.2e+03;
RESULT 945
Query Match 4.1%; Score 31.2; DB 10; Length 110000;
Best Local Similarity 50.7%; Pred. No. 1.2e+03;
RESULT 946

Query Match 4.1%; Score 31.2; DB 12; Length 110000;
Best Local Similarity 47.9%; Pred. No. 1.2e+03;
RESULT 947
ID ADL08109 standard; DNA; 247682 BP.
DE Human gene associated with low HDL-C AT3.
PN US2004043389-A1.
PD 04-MAR-2004.
PA (VITI-) VITIVITY INC.
Query Match 4.1%; Score 31.2; DB 12; Length 247682;
Best Local Similarity 47.9%; Pred. No. 1.6e+03;
RESULT 948
ID ABK89296 standard; DNA; 326014 BP.
DE Human gene for novel serine/threonine serine kinase.
Query Match 4.1%; Score 31.2; DB 6; Length 326014;
Best Local Similarity 60.7%; Pred. No. 1.8e+03;
RESULT 949
ID ADQ94981 standard; DNA; 326014 BP.
DE Human kinase genomic DNA.
Query Match 4.1%; Score 31.2; DB 12; Length 326014;
Best Local Similarity 60.7%; Pred. No. 1.8e+03;
RESULT 950
ID AAC29772 standard; cDNA; 389 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 33847.
PN EPI033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Query Match 4.0%; Score 31; DB 3; Length 389;
Best Local Similarity 57.9%; Pred. No. 96;
RESULT 951
ID ABV06585 standard; cDNA; 393 BP.
DE Human prostate expression marker cDNA 6576.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 31; DB 5; Length 393;
Best Local Similarity 52.8%; Pred. No. 97;
RESULT 952
ID ABX62061 standard; DNA; 429 BP.
DE Arabidopsis thaliana expressed sequence related polynucleotide #176.
PN US2002040490-A1.
PD 04-APR-2002.
PA (GORL/) GORLACH J.
PA (ANY/) AN Y.
PA (HAMI/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (RAIN/) RAINES T M.
PA (YUY/) YU Y.
PA (RAME/) RAMEAKA J G.
PA (PAGE/) PAGE A.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
PA (KRIC/) KRICKER M.
PA (SLAT/) SLATER T.
PA (DAVI/) DAVIS K R.
PA (ALLE/) ALLEN K.
PA (HOFF/) HOFFMAN N.
PA (HURB/) HURBAN P.
Query Match 4.0%; Score 31; DB 8; Length 429;
Best Local Similarity 59.8%; Pred. No. 1e+02;
RESULT 953
ID AAF12938 standard; cDNA; 636 BP.
DE Aspergillus oryzae EST SEQ ID NO:5461.
PN WO200056762-A2.
PD 28-SEP-2000.
PA (NOVO) NOVO NORDISK BIOTECH INC.
PA (NOVO) NOVO NORDISK AS.
Query Match 4.0%; Score 31; DB 3; Length 636;
Best Local Similarity 51.0%; Pred. No. 1.2e+02;
RESULT 954
ID ADN73602 standard; cDNA; 648 BP.

DE Thale cress cDNA repressed in E2Fa/Dpa expressing plants SeqID 1497.
PN WO2004035798-A2.
PD 29-APR-2004.
PA (CROP-) CROPDESIGN NV.
Query Match 4.0%; Score 31; DB 12; Length 648;
Best Local Similarity 59.8%; Pred. No. 1.2e+02;
RESULT 955
ID ABN99075 standard; DNA; 792 BP.
DE Arabidopsis thaliana expressed polynucleotide SEQ ID NO 843.
PN US2002023281-A1.
PD 21-FEB-2002.
PA (GORL/) GORLACH J.
PA (ANY/) AN Y.
PA (HAMI/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (RAIN/) RAINES T M.
PA (YUY/) YU Y.
PA (RAME/) RAMEAKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHEW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
PA (KRIC/) KRICKER M.
PA (SLAT/) SLATER T.
PA (DAVI/) DAVIS K R.
PA (ALLE/) ALLEN K.
PA (HOFF/) HOFFMAN N.
PA (HURB/) HURBAN P.
Query Match 4.0%; Score 31; DB 6; Length 792;
Best Local Similarity 59.8%; Pred. No. 1.3e+02;
RESULT 956
ID AAA02568 standard; cDNA; 1347 BP.
DE Human colon cancer cell line polynucleotide sequence SEQ ID NO:2559.
PN WO9958675-A2.
PD 18-NOV-1999.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 4.0%; Score 31; DB 3; Length 1347;
Best Local Similarity 42.1%; Pred. No. 1.7e+02;
RESULT 957
ID ABN66457 standard; DNA; 1353 BP.
DE Streptococcus polynucleotide SEQ ID NO 827.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 4.0%; Score 31; DB 6; Length 1353;
Best Local Similarity 51.0%; Pred. No. 1.7e+02;
RESULT 958
ID ABL22302 standard; DNA; 2899 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 18379.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.0%; Score 31; DB 4; Length 2899;
Best Local Similarity 46.5%; Pred. No. 2.5e+02;
RESULT 959
ID ABL28608 standard; DNA; 2985 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 37297.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.0%; Score 31; DB 4; Length 2985;
Best Local Similarity 46.5%; Pred. No. 2.5e+02;
RESULT 960
ID AAL41291 standard; cDNA; 3051 BP.
DE cDNA encoding the protein EST1-1089.
PN EP1245671-A1.
PD 02-OCT-2002.
PA (BTGI-) BTG INT LTD.
Query Match 4.0%; Score 31; DB 6; Length 3051;

Best Local Similarity 57.9%; Pred. No. 2.5e+02;
RESULT 961
ID ABV72520 standard; cDNA; 3051 BP.
DE Nucleotide sequence of a human protein designated EST1-1089.
PN WO200277220-A2.
PD 03-OCT-2002.
PA (BTGI-) BTG INT LTD.
Query Match 4.0%; Score 31; DB 8; Length 3051;
Best Local Similarity 57.9%; Pred. No. 2.5e+02;
RESULT 962
ID ABL08882 standard; cDNA; 3658 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 21128.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.0%; Score 31; DB 4; Length 3658;
Best Local Similarity 59.8%; Pred. No. 2.7e+02;
RESULT 963
ID AAF29637 standard; DNA; 5429 BP.
DE Arabidopsis thaliana fwa gene.
PN WO200102573-A1.
PD 11-JAN-2001.
PA (UYWA-) UNIV WAGENINGEN.
Query Match 4.0%; Score 31; DB 5; Length 5429;
Best Local Similarity 50.3%; Pred. No. 3.3e+02;
RESULT 964
ID AAF29556 standard; DNA; 5429 BP.
DE Arabidopsis thaliana ecotype Landsberg erecta FWA-1 gene.
PN WO200102572-A1.
PD 11-JAN-2001.
PA (UYWA-) UNIV WAGENINGEN.
Query Match 4.0%; Score 31; DB 5; Length 5429;
Best Local Similarity 50.3%; Pred. No. 3.3e+02;
RESULT 965
ID ABA19876 standard; DNA; 8588 BP.
DE Human nervous system related polynucleotide SEQ ID NO 12207.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.0%; Score 31; DB 5; Length 8588;
Best Local Similarity 50.3%; Pred. No. 4.1e+02;
RESULT 966
ID ABA16043 standard; DNA; 8588 BP.
DE Human nervous system related polynucleotide SEQ ID NO 8374.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.0%; Score 31; DB 5; Length 8588;
Best Local Similarity 50.3%; Pred. No. 4.1e+02;
RESULT 967
Query Match 4.0%; Score 31; DB 6; Length 110000;
Best Local Similarity 51.0%; Pred. No. 1.3e+03;
RESULT 968
ID AAD62832 standard; DNA; 180216 BP.
DE Human BAC #1 containing formin (Fmn)-2 genomic DNA.
PN US2003170683-A1.
PD 11-SEP-2003.
PA (LEDE/) LEADER P.
PA (LEAD/) LEADER B.
Query Match 4.0%; Score 31; DB 10; Length 180216;
Best Local Similarity 49.1%; Pred. No. 1.6e+03;
RESULT 969
ID ABV15242 standard; cDNA; 265 BP.
DE Human prostate expression marker cDNA 15233.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 265;
Best Local Similarity 53.3%; Pred. No. 92;
RESULT 970
ID ABV06073 standard; cDNA; 285 BP.
DE Human prostate expression marker cDNA 6064.
PN WO200160860-A2.

PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 285;
Best Local Similarity 53.3%; Pred. No. 96;
RESULT 971
ID ABV02501 standard; cDNA; 303 BP.
DE Human prostate expression marker cDNA 2492.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 303;
Best Local Similarity 53.3%; Pred. No. 98;
RESULT 972
ID ABV06050 standard; cDNA; 323 BP.
DE Human prostate expression marker cDNA 6041.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 323;
Best Local Similarity 53.3%; Pred. No. 1e+02;
RESULT 973
ID ABV00225 standard; cDNA; 327 BP.
DE Human prostate expression marker cDNA 216.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 327;
Best Local Similarity 53.3%; Pred. No. 1e+02;
RESULT 974
ID ABV00462 standard; cDNA; 328 BP.
DE Human prostate expression marker cDNA 453.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 328;
Best Local Similarity 53.3%; Pred. No. 1e+02;
RESULT 975
ID ABV11345 standard; cDNA; 331 BP.
DE Human prostate expression marker cDNA 11336.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 331;
Best Local Similarity 53.3%; Pred. No. 1e+02;
RESULT 976
ID ABV15219 standard; cDNA; 341 BP.
DE Human prostate expression marker cDNA 15210.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 341;
Best Local Similarity 53.3%; Pred. No. 1e+02;
RESULT 977
ID ABV07323 standard; cDNA; 344 BP.
DE Human prostate expression marker cDNA 7314.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 344;
Best Local Similarity 53.3%; Pred. No. 1e+02;
RESULT 978
ID ABV15215 standard; cDNA; 346 BP.
DE Human prostate expression marker cDNA 15206.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 346;
Best Local Similarity 53.3%; Pred. No. 1e+02;
RESULT 979
ID ABV09631 standard; cDNA; 346 BP.
DE Human prostate expression marker cDNA 9622.
PN WO200160860-A2.
PD 23-AUG-2001.

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PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 346;
Best Local Similarity 53.3%; Pred. No. 1e+02;
RESULT 980
ID ABV02913 standard; cDNA; 355 BP.
DE Human prostate expression marker cDNA 2904.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 355;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 981
ID ABV12082 standard; cDNA; 356 BP.
DE Human prostate expression marker cDNA 12073.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 356;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 982
ID ABV10258 standard; cDNA; 361 BP.
DE Human prostate expression marker cDNA 10249.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 361;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 983
ID ABV02365 standard; cDNA; 362 BP.
DE Human prostate expression marker cDNA 2356.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 362;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 984
ID ABV06786 standard; cDNA; 363 BP.
DE Human prostate expression marker cDNA 6777.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 363;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 985
ID ABV09020 standard; cDNA; 366 BP.
DE Human prostate expression marker cDNA 9011.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 366;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 986
ID ABV11534 standard; cDNA; 372 BP.
DE Human prostate expression marker cDNA 11525.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 372;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 987
ID ABV11804 standard; cDNA; 374 BP.
DE Human prostate expression marker cDNA 11795.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 374;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 988
ID ABV11780 standard; cDNA; 374 BP.
DE Human prostate expression marker cDNA 11771.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 374;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 989
ID ABV12165 standard; cDNA; 374 BP.
DE Human prostate expression marker cDNA 12156.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 374;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 990
ID ABV10423 standard; cDNA; 376 BP.
DE Human prostate expression marker cDNA 10414.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 376;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 991
ID ABV02635 standard; cDNA; 380 BP.
DE Human prostate expression marker cDNA 2626.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 380;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 992
ID ABV10172 standard; cDNA; 381 BP.
DE Human prostate expression marker cDNA 10163.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 381;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 993
ID ABV02732 standard; cDNA; 381 BP.
DE Human prostate expression marker cDNA 2723.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 381;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 994
ID ABV36014 standard; cDNA; 383 BP.
DE Human prostate expression marker cDNA 36005.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 383;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 995
ID ABV32490 standard; cDNA; 383 BP.
DE Human prostate expression marker cDNA 32481.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 383;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 996
ID ABV11707 standard; cDNA; 383 BP.
DE Human prostate expression marker cDNA 11698.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 383;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 997
ID ABV11541 standard; cDNA; 385 BP.
DE Human prostate expression marker cDNA 11532.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 385;
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Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 998
ID ABV32815 standard; cDNA; 385 BP.
DE Human prostate expression marker cDNA 32806.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
Length 385;
RESULT 999
ID ABV10522 standard; cDNA; 388 BP.
DE Human prostate expression marker cDNA 10513.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
Length 388;
RESULT 1000
ID ABV02996 standard; cDNA; 390 BP.
DE Human prostate expression marker cDNA 2987.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
Length 390;
RESULT 1001
ID ABV11670 standard; cDNA; 391 BP.
DE Human prostate expression marker cDNA 11661.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
Length 391;
RESULT 1002
ID ABV11899 standard; cDNA; 391 BP.
DE Human prostate expression marker cDNA 11890.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
Length 391;
RESULT 1003
ID ABV02734 standard; cDNA; 391 BP.
DE Human prostate expression marker cDNA 2725.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
Length 391;
RESULT 1004
ID ABV31270 standard; cDNA; 392 BP.
DE Human prostate expression marker cDNA 31261.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
Length 392;
RESULT 1005
ID ABV11903 standard; cDNA; 393 BP.
DE Human prostate expression marker cDNA 11894.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
Length 393;
RESULT 1006
ID ABV15400 standard; cDNA; 395 BP.
DE Human prostate expression marker cDNA 15391.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
Length 395;
RESULT 997
ID ABV11821 standard; cDNA; 396 BP.
DE Human prostate expression marker cDNA 11812.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
Length 396;
RESULT 1008
ID ABV11947 standard; cDNA; 397 BP.
DE Human prostate expression marker cDNA 11938.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
Length 397;
RESULT 1009
ID ABV11555 standard; cDNA; 398 BP.
DE Human prostate expression marker cDNA 11546.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
Length 398;
RESULT 1010
ID ABV11901 standard; cDNA; 398 BP.
DE Human prostate expression marker cDNA 11892.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
Length 398;
RESULT 1011
ID ABV12026 standard; cDNA; 399 BP.
DE Human prostate expression marker cDNA 12017.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
Length 399;
RESULT 1012
ID ABV02814 standard; cDNA; 400 BP.
DE Human prostate expression marker cDNA 2805.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
Length 400;
RESULT 1013
ID ABV32679 standard; cDNA; 401 BP.
DE Human prostate expression marker cDNA 32670.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
Length 401;
RESULT 1014
ID ABV11712 standard; cDNA; 401 BP.
DE Human prostate expression marker cDNA 11703.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
Length 401;
RESULT 1015
ID ABV43873 standard; cDNA; 402 BP.
DE Human prostate expression marker cDNA 43864.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
Length 402;
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ID ABV02909 standard; cDNA; 402 BP.
DE Human prostate expression marker cDNA 2900.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 402;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 1017
ID ABV31429 standard; cDNA; 402 BP.
DE Human prostate expression marker cDNA 31420.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 402;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 1018
ID ABV11983 standard; cDNA; 402 BP.
DE Human prostate expression marker cDNA 11974.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 402;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 1019
ID ABV02538 standard; cDNA; 406 BP.
DE Human prostate expression marker cDNA 2529.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 402;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 1020
ID ABV11825 standard; cDNA; 406 BP.
DE Human prostate expression marker cDNA 11816.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 406;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 1021
ID ABV33227 standard; cDNA; 407 BP.
DE Human prostate expression marker cDNA 33218.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 407;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 1022
ID ABV42150 standard; cDNA; 407 BP.
DE Human prostate expression marker cDNA 42141.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 407;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 1023
ID ABV02386 standard; cDNA; 407 BP.
DE Human prostate expression marker cDNA 2377.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 407;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 1024
ID ABV12163 standard; cDNA; 410 BP.
DE Human prostate expression marker cDNA 12154.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 410;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 1025
ID ABV10237 standard; cDNA; 410 BP.
DE Human prostate expression marker cDNA 10228.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 410;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 1026
ID ABV36018 standard; cDNA; 411 BP.
DE Human prostate expression marker cDNA 36009.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 411;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 1027
ID ABV06231 standard; cDNA; 411 BP.
DE Human prostate expression marker cDNA 6222.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 411;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 1028
ID ABV32925 standard; cDNA; 414 BP.
DE Human prostate expression marker cDNA 32916.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 414;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 1029
ID ABV41850 standard; cDNA; 414 BP.
DE Human prostate expression marker cDNA 41841.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 414;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 1030
ID ABV32852 standard; cDNA; 416 BP.
DE Human prostate expression marker cDNA 32843.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 416;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 1031
ID ABV02857 standard; cDNA; 416 BP.
DE Human prostate expression marker cDNA 2848.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 416;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 1032
ID ABV02730 standard; cDNA; 417 BP.
DE Human prostate expression marker cDNA 2721.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 417;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 1033
ID ABV33310 standard; cDNA; 418 BP.
DE Human prostate expression marker cDNA 33301.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 418;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 1034
ID ABV42233 standard; cDNA; 418 BP.
DE Human prostate expression marker cDNA 42224.
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PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 418;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 1035
ID ABV45074 standard; cDNA; 419 BP.
DE Human prostate expression marker cDNA 45065.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 419;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 1036
ID ABV01003 standard; cDNA; 419 BP.
DE Human prostate expression marker cDNA 994.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 419;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 1037
ID ABV31593 standard; cDNA; 419 BP.
DE Human prostate expression marker cDNA 31584.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 419;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 1038
ID ABV32686 standard; cDNA; 419 BP.
DE Human prostate expression marker cDNA 32677.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 419;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 1039
ID ABV41777 standard; cDNA; 419 BP.
DE Human prostate expression marker cDNA 41768.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 419;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 1040
ID ABV32949 standard; cDNA; 421 BP.
DE Human prostate expression marker cDNA 32940.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 421;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 1041
ID ABV01254 standard; cDNA; 421 BP.
DE Human prostate expression marker cDNA 1245.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 421;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 1042
ID ABV12282 standard; cDNA; 422 BP.
DE Human prostate expression marker cDNA 12273.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 422;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 1043
ID ABV31343 standard; cDNA; 422 BP.
DE Human prostate expression marker cDNA 31334.
PN WO200160860-A2.

PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 422;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 1044
ID ABV02652 standard; cDNA; 423 BP.
DE Human prostate expression marker cDNA 2643.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 423;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
RESULT 1045
ID ABK39114 standard; cDNA; 427 BP.
DE cDNA encoding lung tumour protein clone R0130:G12.
PN WO200204514-A2.
PD 17-JAN-2002.
PA (CORI-) CORIXA CORP.
Query Match 4.0%; Score 30.8; DB 6; Length 427;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
RESULT 1046
ID AC11443 standard; cDNA; 427 BP.
DE Human lung adenocarcinoma library cDNA SEQ ID 1152.
PN US2002197669-A1.
PD 26-DEC-2002.
PA (BANG/) BANGUR C S.
PA (FANG/) FANGER G R.
PA (WANG/) WANG A.
PA (WANG/) WANG T.
PA (SWIT/) SWITZER A P.
PA (MCNE/) MCNEILL P D.
PA (CLAP/) CLAPPER J D.
Query Match 4.0%; Score 30.8; DB 8; Length 427;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
RESULT 1047
ID ACA02629 standard; cDNA; 427 BP.
DE Lung cancer therapyand diagnosis associated cDNA #1118.
PN US2002172952-A1.
PD 21-NOV-2002.
PA (CORI-) CORIXA CORP.
Query Match 4.0%; Score 30.8; DB 8; Length 427;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
RESULT 1048
ID ADH46671 standard; cDNA; 427 BP.
DE Human lung tumour cDNA clone, SEQ ID No 1152.
PN WO2003037267-A2.
PD 08-MAY-2003.
PA (CORI-) CORIXA CORP.
Query Match 4.0%; Score 30.8; DB 10; Length 427;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
RESULT 1049
ID ABV33044 standard; cDNA; 428 BP.
DE Human prostate expression marker cDNA 33035.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 428;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1050
ID ABV41969 standard; cDNA; 428 BP.
DE Human prostate expression marker cDNA 41960.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 428;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1051
ID ABV02974 standard; cDNA; 429 BP.
DE Human prostate expression marker cDNA 2965.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5; Length 429;
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Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1052
ID ABV03113 standard; cDNA; 429 BP.
DE Human prostate expression marker cDNA 3104.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
Length 429;
RESULT 1053
ID ABV12143 standard; cDNA; 430 BP.
DE Human prostate expression marker cDNA 12134.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
Length 430;
RESULT 1054
ID ABV12193 standard; cDNA; 432 BP.
DE Human prostate expression marker cDNA 12184.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
Length 432;
RESULT 1055
ID ABV33048 standard; cDNA; 432 BP.
DE Human prostate expression marker cDNA 33039.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
Length 432;
RESULT 1056
ID ABV32966 standard; cDNA; 434 BP.
DE Human prostate expression marker cDNA 32957.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
Length 434;
RESULT 1057
ID ABV31692 standard; cDNA; 434 BP.
DE Human prostate expression marker cDNA 31683.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
Length 434;
RESULT 1058
ID ABV03024 standard; cDNA; 435 BP.
DE Human prostate expression marker cDNA 3015.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
Length 435;
RESULT 1059
ID ABV32857 standard; cDNA; 435 BP.
DE Human prostate expression marker cDNA 32848.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
Length 435;
RESULT 1060
ID ABV42053 standard; cDNA; 435 BP.
DE Human prostate expression marker cDNA 42044.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
Length 435;

RESULT 1061
ID ABV33128 standard; cDNA; 435 BP.
DE Human prostate expression marker cDNA 33119.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
Length 435;
RESULT 1062
ID ABV07053 standard; cDNA; 438 BP.
DE Human prostate expression marker cDNA 7044.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
Length 438;
RESULT 1063
ID ABV36192 standard; cDNA; 439 BP.
DE Human prostate expression marker cDNA 36183.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
Length 439;
RESULT 1064
ID ABV45244 standard; cDNA; 439 BP.
DE Human prostate expression marker cDNA 45235.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
Length 439;
RESULT 1065
ID ABV33092 standard; cDNA; 440 BP.
DE Human prostate expression marker cDNA 33083.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
Length 440;
RESULT 1066
ID ABV42017 standard; cDNA; 440 BP.
DE Human prostate expression marker cDNA 42008.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
Length 440;
RESULT 1067
ID ABV41782 standard; cDNA; 440 BP.
DE Human prostate expression marker cDNA 41773.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
Length 440;
RESULT 1068
ID ABV36995 standard; cDNA; 441 BP.
DE Human prostate expression marker cDNA 36986.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
Length 441;
RESULT 1069
ID ABV41874 standard; cDNA; 441 BP.
DE Human prostate expression marker cDNA 41865.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
Length 441;
RESULT 1070

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ID ABV02372 standard; cDNA; 441 BP.
DE Human prostate expression marker cDNA 2363.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1071 Length 441;
ID ABV36732 standard; cDNA; 442 BP.
DE Human prostate expression marker cDNA 36723.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1072 Length 442;
ID ABV32700 standard; cDNA; 443 BP.
DE Human prostate expression marker cDNA 32691.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1073 Length 443;
ID ABV41740 standard; cDNA; 443 BP.
DE Human prostate expression marker cDNA 41731.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1074 Length 443;
ID ABV41805 standard; cDNA; 443 BP.
DE Human prostate expression marker cDNA 41796.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1075 Length 443;
ID ABV02778 standard; cDNA; 445 BP.
DE Human prostate expression marker cDNA 2769.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1076 Length 445;
ID ABV42095 standard; cDNA; 446 BP.
DE Human prostate expression marker cDNA 42086.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1077 Length 446;
ID ABV41846 standard; cDNA; 446 BP.
DE Human prostate expression marker cDNA 41837.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1078 Length 446;
ID ABV33171 standard; cDNA; 446 BP.
DE Human prostate expression marker cDNA 33162.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1079 Length 446;
ID ABV32970 standard; cDNA; 447 BP.
DE Human prostate expression marker cDNA 40552.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1080 Length 447;
ID ABV02656 standard; cDNA; 450 BP.
DE Human prostate expression marker cDNA 2647.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1081 Length 450;
ID ABV31408 standard; cDNA; 452 BP.
DE Human prostate expression marker cDNA 31399.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1082 Length 452;
ID ABV40377 standard; cDNA; 452 BP.
DE Human prostate expression marker cDNA 40368.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1083 Length 452;
ID ABV01068 standard; cDNA; 453 BP.
DE Human prostate expression marker cDNA 1059.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1084 Length 453;
ID ABV33427 standard; cDNA; 462 BP.
DE Human prostate expression marker cDNA 33418.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1085 Length 462;
ID ABV33308 standard; cDNA; 463 BP.
DE Human prostate expression marker cDNA 33299.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1086 Length 463;
ID ABV33288 standard; cDNA; 464 BP.
DE Human prostate expression marker cDNA 33279.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1087 Length 464;
ID ABV40312 standard; cDNA; 464 BP.
DE Human prostate expression marker cDNA 40303.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1088 Length 464;
ID ABV40561 standard; cDNA; 464 BP.
DE Human prostate expression marker cDNA 40552.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1089 Length 464;
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PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1089 Length 464;
ID ABV40660 standard; cDNA; 464 BP.
DE Human prostate expression marker cDNA 40651.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1090 Length 464;
ID ABV45053 standard; cDNA; 464 BP.
DE Human prostate expression marker cDNA 45044.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1091 Length 464;
ID ABV42211 standard; cDNA; 464 BP.
DE Human prostate expression marker cDNA 42202.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1092 Length 464;
ID ABV40398 standard; cDNA; 468 BP.
DE Human prostate expression marker cDNA 40389.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1093 Length 468;
ID ABV33338 standard; cDNA; 468 BP.
DE Human prostate expression marker cDNA 33329.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1094 Length 468;
ID ABV45078 standard; cDNA; 469 BP.
DE Human prostate expression marker cDNA 45069.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1095 Length 469;
ID ABV33443 standard; cDNA; 469 BP.
DE Human prostate expression marker cDNA 33434.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1096 Length 469;
ID ABV42366 standard; cDNA; 469 BP.
DE Human prostate expression marker cDNA 42357.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1097 Length 469;
ID ABV06651 standard; cDNA; 496 BP.
DE Human prostate expression marker cDNA 6642.
PN WO200160860-A2.

PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1098 Length 496;
ID ABV60369 standard; cDNA; 504 BP.
DE Human prostate expression marker cDNA 60360.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
RESULT 1099 Length 504;
ID ABV39172 standard; cDNA; 517 BP.
DE Human prostate expression marker cDNA 39163.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.3e+02;
RESULT 1100 Length 517;
ID ABV36599 standard; cDNA; 520 BP.
DE Human prostate expression marker cDNA 36590.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.3e+02;
RESULT 1101 Length 520;
ID ABV41604 standard; cDNA; 520 BP.
DE Human prostate expression marker cDNA 41595.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.3e+02;
RESULT 1102 Length 520;
ID ABV06802 standard; cDNA; 541 BP.
DE Human prostate expression marker cDNA 6793.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.3e+02;
RESULT 1103 Length 541;
ID ABV02706 standard; cDNA; 565 BP.
DE Human prostate expression marker cDNA 2697.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.3e+02;
RESULT 1104 Length 565;
ID ABV03129 standard; cDNA; 569 BP.
DE Human prostate expression marker cDNA 3120.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.3e+02;
RESULT 1105 Length 569;
ID ADI72125 standard; DNA; 578 BP.
DE Human ovarian cancer DNA marker #4867.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.3e+02;
RESULT 1106 Length 578;
ID ADL37274 standard; DNA; 578 BP.
DE Human ovarian cancer DNA marker #11164.
PN WO200170979-A2.
PD 27-SEP-2001.


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PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 41.3%; Pred. No. 1.3e+02;
RESULT 1107 Length 578;
ID ABV42146 standard; cDNA; 602 BP.
DE Human prostate expression marker cDNA 42137.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.4e+02;
RESULT 1108 Length 602;
ID ABV41895 standard; cDNA; 602 BP.
DE Human prostate expression marker cDNA 41886.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.4e+02;
RESULT 1109 Length 602;
ID ABV39454 standard; cDNA; 602 BP.
DE Human prostate expression marker cDNA 39445.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.4e+02;
RESULT 1110 Length 602;
ID ABV37259 standard; cDNA; 602 BP.
DE Human prostate expression marker cDNA 37250.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.4e+02;
RESULT 1111 Length 602;
ID ABV36748 standard; cDNA; 602 BP.
DE Human prostate expression marker cDNA 36739.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.4e+02;
RESULT 1112 Length 602;
ID ABV41891 standard; cDNA; 602 BP.
DE Human prostate expression marker cDNA 41882.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.4e+02;
RESULT 1113 Length 602;
ID ABV41419 standard; cDNA; 602 BP.
DE Human prostate expression marker cDNA 41410.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.4e+02;
RESULT 1114 Length 602;
ID ABV43273 standard; cDNA; 602 BP.
DE Human prostate expression marker cDNA 43264.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.4e+02;
RESULT 1115 Length 602;
ID ABV33046 standard; cDNA; 602 BP.
DE Human prostate expression marker cDNA 33037.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.4e+02;
RESULT 1116 Length 602;
ID ABV41973 standard; cDNA; 602 BP.
DE Human prostate expression marker cDNA 41964.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.4e+02;
RESULT 1117 Length 602;
ID ABV42261 standard; cDNA; 602 BP.
DE Human prostate expression marker cDNA 42252.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.4e+02;
RESULT 1118 Length 602;
ID ABV41971 standard; cDNA; 602 BP.
DE Human prostate expression marker cDNA 41962.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.4e+02;
RESULT 1119 Length 602;
ID ABV41611 standard; cDNA; 602 BP.
DE Human prostate expression marker cDNA 41602.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.4e+02;
RESULT 1120 Length 602;
ID ABV42231 standard; cDNA; 602 BP.
DE Human prostate expression marker cDNA 42222.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.4e+02;
RESULT 1121 Length 602;
ID ABV42350 standard; cDNA; 602 BP.
DE Human prostate expression marker cDNA 42341.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.4e+02;
RESULT 1122 Length 602;
ID ABV41625 standard; cDNA; 602 BP.
DE Human prostate expression marker cDNA 41616.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.4e+02;
RESULT 1123 Length 602;
ID ABV09048 standard; cDNA; 603 BP.
DE Human prostate expression marker cDNA 9039.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.4e+02;
RESULT 1124 Length 603;
ID ABV12298 standard; cDNA; 689 BP.
DE Human prostate expression marker cDNA 12289.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.8; DB 5;
Best Local Similarity 53.3%; Pred. No. 1.4e+02;
RESULT 1125 Length 689;
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Best Local Similarity 53.3%; Pred. No. 1.4e+02;
RESULT 1125
ID AAC54777 standard; DNA; 769 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 79053.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 4.0%; Score 30.8; DB 3; Length 769;
Best Local Similarity 48.3%; Pred. No. 1.5e+02;
RESULT 1126
ID AAC52294 standard; DNA; 771 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 70880.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 4.0%; Score 30.8; DB 3; Length 771;
Best Local Similarity 48.3%; Pred. No. 1.5e+02;
RESULT 1127
ID AAV06562 standard; cDNA; 2248 BP.
DE Arabidopsis cellulose synthase EST T20782 cDNA.
PN WO9800549-A1.
PD 08-JAN-1998.
PA (AUSU ) UNIV AUSTRALIAN NAT.
PA (CSIR ) COMMONWEALTH SCI & IND RES ORG.
Query Match 4.0%; Score 30.8; DB 2; Length 2248;
Best Local Similarity 54.4%; Pred. No. 2.5e+02;
RESULT 1128
ID ABK42634 standard; DNA; 3877 BP.
DE Genomic sequence #533 encoding novel human connective tissue polypeptide.
PN WO200155343-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.0%; Score 30.8; DB 4; Length 3877;
Best Local Similarity 51.4%; Pred. No. 3.2e+02;
RESULT 1129
ID ABA20095 standard; DNA; 3877 BP.
DE Human nervous system related polynucleotide SEQ ID NO 12426.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.0%; Score 30.8; DB 5; Length 3877;
Best Local Similarity 51.4%; Pred. No. 3.2e+02;
RESULT 1130
ID ADB60790 standard; DNA; 3877 BP.
DE Connective tissue related genomic DNA #533.
PN US2003054375-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.0%; Score 30.8; DB 9; Length 3877;
Best Local Similarity 51.4%; Pred. No. 3.2e+02;
RESULT 1131
ID ABK42632 standard; DNA; 3879 BP.
DE Genomic sequence #531 encoding novel human connective tissue polypeptide.
PN WO200155343-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.0%; Score 30.8; DB 4; Length 3879;
Best Local Similarity 51.4%; Pred. No. 3.2e+02;
RESULT 1132
ID ADB60788 standard; DNA; 3879 BP.
DE Connective tissue related genomic DNA #531.
PN US2003054375-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.0%; Score 30.8; DB 9; Length 3879;
Best Local Similarity 51.4%; Pred. No. 3.2e+02;
RESULT 1133
ID AAX55607 standard; DNA; 3960 BP.
DE Human clone 65 antisense sequence.
PN WO9921999-A2.
PD 06-MAY-1999.
PA (GETH ) GENENTECH INC.
Query Match 4.0%; Score 30.8; DB 2; Length 3960;
Best Local Similarity 55.7%; Pred. No. 3.3e+02;
RESULT 1134
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ID AAX55606 standard; DNA; 3960 BP.
DE Human clone 65 protein encoding DNA.
PN WO9921999-A2.
PD 06-MAY-1999.
PA (GETH ) GENENTECH INC.
Query Match 4.0%; Score 30.8; DB 2; Length 3960;
Best Local Similarity 55.7%; Pred. No. 3.3e+02;
RESULT 1135
ID ACF64329 standard; DNA; 5148 BP.
DE Human ESR1 nucleotide sequence >ESR1_07.
PN WO2003014319-A2.
PD 20-FEB-2003.
PA (DNAS-) DNA SCI INC.
Query Match 4.0%; Score 30.8; DB 8; Length 5148;
Best Local Similarity 57.6%; Pred. No. 3.7e+02;
RESULT 1136
ID AAS61416 standard; DNA; 5887 BP.
DE Human gene regulation-associated gene oligonucleotide #371.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.0%; Score 30.8; DB 6; Length 5887;
Best Local Similarity 55.7%; Pred. No. 3.9e+02;
RESULT 1137
ID AAD28372 standard; DNA; 6175 BP.
DE Human chemically treated genomic DNA #13.
PN WO200202809-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.0%; Score 30.8; DB 6; Length 6175;
Best Local Similarity 47.0%; Pred. No. 4e+02;
RESULT 1138
ID ADA69607 standard; DNA; 6477 BP.
DE Rice gene, SEQ ID 2930.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.
Query Match 4.0%; Score 30.8; DB 8; Length 6477;
Best Local Similarity 47.8%; Pred. No. 4.1e+02;
RESULT 1139
ID ABN80082 standard; DNA; 10250 BP.
DE Human chemically modified disease associated gene SEQ ID NO 99.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.0%; Score 30.8; DB 6; Length 10250;
Best Local Similarity 48.8%; Pred. No. 5.1e+02;
RESULT 1140
ID ABL33544 standard; DNA; 10328 BP.
DE Human immune system associated gene SEQ ID NO: 1517.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.0%; Score 30.8; DB 6; Length 10328;
Best Local Similarity 52.3%; Pred. No. 5.1e+02;
RESULT 1141
ID ABL32281 standard; DNA; 13511 BP.
DE Human immune system associated gene SEQ ID NO: 254.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.0%; Score 30.8; DB 6; Length 13511;
Best Local Similarity 46.7%; Pred. No. 5.8e+02;
RESULT 1142
ID ABL05454 standard; cDNA; 13815 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 10844.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Query Match 4.0%; Score 30.8; DB 4; Length 13815;
Best Local Similarity 61.0%; Pred. No. 5.9e+02;
RESULT 1143
ID ABL70460 standard; DNA; 16228 BP.
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DE Chemically treated cell signalling DNA sequence complementary to#175.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.0%; Score 30.8; DB 6; Length 16228;
Best Local Similarity 45.7%; Pred. No. 6.3e+02;
RESULT 1144
ID AAS61425 standard; DNA; 16228 BP.
DE Human gene regulation-associated gene oligonucleotide #380.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.0%; Score 30.8; DB 6; Length 16228;
Best Local Similarity 45.7%; Pred. No. 6.3e+02;
RESULT 1145
ID ADA02753 standard; DNA; 54355 BP.
DE Mouse Morf carcinoma associated gene, SEQ ID NO:1271.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 4.0%; Score 30.8; DB 9; Length 54355;
Best Local Similarity 54.4%; Pred. No. 1.1e+03;
RESULT 1146
ID ADB72491 standard; DNA; 54355 BP.
DE Mouse Morf gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 4.0%; Score 30.8; DB 10; Length 54355;
Best Local Similarity 54.4%; Pred. No. 1.1e+03;
RESULT 1147
ID ADC85233 standard; DNA; 54355 BP.
DE Mouse Morf genomic sequence.
PN WO2003045230-A2.
PD 05-JUN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 4.0%; Score 30.8; DB 10; Length 54355;
Best Local Similarity 54.4%; Pred. No. 1.1e+03;
RESULT 1148
ID ADM74348 standard; DNA; 54355 BP.
DE Murine carcinoma associated (CA) nucleic acid #10.
PN US2004072154-A1.
PD 15-APR-2004.
PA (MORR/) MORRIS D W.
PA (ENGE/) ENGELHARD E K.
Query Match 4.0%; Score 30.8; DB 12; Length 54355;
Best Local Similarity 54.4%; Pred. No. 1.1e+03;
RESULT 1149
ID ABL12402 standard; cDNA; 90104 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 31688.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.0%; Score 30.8; DB 4; Length 90104;
Best Local Similarity 46.0%; Pred. No. 1.4e+03;
RESULT 1150
ID ADH51151 standard; DNA; 151830 BP.
DE Protein phosphatase 2A beta-gamma subunit PPP2R2C gene.
PN WO2004001068-A2.
PD 31-DEC-2003.
PA (GEST) GENSET SA.
Query Match 4.0%; Score 30.8; DB 12; Length 151830;
Best Local Similarity 76.0%; Pred. No. 1.8e+03;
RESULT 1151
ID ADM78027 standard; DNA; 151830 BP.
DE Human PPP2R2C genomic DNA.
PN WO2004000875-A2.
PD 31-DEC-2003.
PA (GEST) GENSET SA.
Query Match 4.0%; Score 30.8; DB 12; Length 151830;
Best Local Similarity 76.0%; Pred. No. 1.8e+03;
RESULT 1152
ID ADF51132 standard; DNA; 243428 BP.

DE Human P-Rex1 genomic DNA sequence.
PN WO2003080664-A1.
PD 02-OCT-2003.
PA (BABR-) BABRAHAM INST.
Query Match 4.0%; Score 30.8; DB 12; Length 243428;
Best Local Similarity 57.1%; Pred. No. 2.1e+03;
RESULT 1153
ID AAC27654 standard; cDNA; 347 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 31729.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Query Match 4.0%; Score 30.6; DB 3; Length 347;
Best Local Similarity 52.1%; Pred. No. 1.2e+02;
RESULT 1154
ID AAF18350 standard; DNA; 428 BP.
DE Lung cancer associated polynucleotide sequence SEQ ID 369.
PN WO200055180-A2.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
Query Match 4.0%; Score 30.6; DB 3; Length 428;
Best Local Similarity 57.4%; Pred. No. 1.3e+02;
RESULT 1155
ID AAS83465 standard; cDNA; 433 BP.
DE DNA encoding novel human diagnostic protein #19269.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.0%; Score 30.6; DB 5; Length 433;
Best Local Similarity 52.8%; Pred. No. 1.3e+02;
RESULT 1156
ID AAH11396 standard; cDNA; 532 BP.
DE Human cDNA clone (3'-primer) SEQ ID NO:8231.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 4.0%; Score 30.6; DB 4; Length 532;
Best Local Similarity 48.9%; Pred. No. 1.5e+02;
RESULT 1157
ID AAS67705 standard; cDNA; 608 BP.
DE DNA encoding novel human diagnostic protein #3509.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.0%; Score 30.6; DB 5; Length 608;
Best Local Similarity 52.8%; Pred. No. 1.6e+02;
RESULT 1158
ID ABN61662 standard; cDNA; 618 BP.
DE Human cancer related polynucleotide SEQ ID NO 1629.
PN WO200214500-A2.
PD 21-FEB-2002.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 4.0%; Score 30.6; DB 6; Length 618;
Best Local Similarity 46.2%; Pred. No. 1.6e+02;
RESULT 1159
ID ABZ12834 standard; DNA; 678 BP.
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 639.
PN WO200216655-A2.
PD 28-FEB-2002.
PA (SCRI) SCRIPPS RES INST.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 4.0%; Score 30.6; DB 6; Length 678;
Best Local Similarity 58.1%; Pred. No. 1.6e+02;
RESULT 1160
ID AAH31554 standard; cDNA; 688 BP.
DE Human olfactory receptor polynucleotide, SEQ ID NO: 127.
PN WO200127158-A2.
PD 19-APR-2001.
PA (DIGI-) DIGISCENTS.
PA (YEDA) YEDA RES & DEV CO LTD.
Query Match 4.0%; Score 30.6; DB 4; Length 688;

Best Local Similarity 50.0%; Pred. No. 1.7e+02;
RESULT 1161
ID AAS80716 standard; cDNA; 966 BP.
DE DNA encoding novel human diagnostic protein #16520.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.0%; Score 30.6; DB 5; Length 966;
Best Local Similarity 48.1%; Pred. No. 1.9e+02;
RESULT 1162
ID ADE55607 standard; DNA; 990 BP.
DE Rat gene AJ007632, SEQ ID NO 1426.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 4.0%; Score 30.6; DB 10; Length 990;
Best Local Similarity 48.1%; Pred. No. 2e+02;
RESULT 1163
ID ADE55605 standard; DNA; 990 BP.
DE Rat gene AJ007632, SEQ ID NO 1424.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 4.0%; Score 30.6; DB 10; Length 990;
Best Local Similarity 48.1%; Pred. No. 2e+02;
RESULT 1164
ID ADA71680 standard; DNA; 1167 BP.
DE Rice gene, SEQ ID 5004.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 4.0%; Score 30.6; DB 8; Length 1167;
Best Local Similarity 30.6%; Pred. No. 2.1e+02;
RESULT 1165
ID ABX72215 standard; cDNA; 1251 BP.
DE Human NOVX polynucleotide #46.
PN WO200281498-A2.
PD 17-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match 4.0%; Score 30.6; DB 8; Length 1251;
Best Local Similarity 53.8%; Pred. No. 2.2e+02;
RESULT 1166
ID ABZ11583 standard; cDNA; 1354 BP.
DE Human polynucleotide SEQ ID NO 465.
PN WO200270539-A2.
PD 12-SEP-2002.
PA (HYSE-) HYSEQ INC.
Query Match 4.0%; Score 30.6; DB 6; Length 1354;
Best Local Similarity 47.2%; Pred. No. 2.3e+02;
RESULT 1167
ID ADM44101 standard; cDNA; 1354 BP.
DE Novel human arginine-rich protein cDNA #465.
PN US2004053250-A1.
PD 18-MAR-2004.
PA (TANG/) TANG Y T.
PA (XUEA/) XUE A.
PA (DRMA/) DRMANAC R T.
Query Match 4.0%; Score 30.6; DB 12; Length 1354;
Best Local Similarity 47.2%; Pred. No. 2.3e+02;
RESULT 1168
ID ADK57600 standard; DNA; 1803 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #4983.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOWC) DOW CHEM CO.
PA (DOWC) DOW AGROSCIENCES LLC.
Query Match 4.0%; Score 30.6; DB 10; Length 1803;
Best Local Similarity 62.3%; Pred. No. 2.6e+02;
RESULT 1169
ID AAC45222 standard; DNA; 1812 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 45735.

PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.0%; Score 30.6; DB 3; Length 1812;
Best Local Similarity 56.4%; Pred. No. 2.6e+02;
RESULT 1170
ID AAC36973 standard; DNA; 1812 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 15728.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.0%; Score 30.6; DB 3; Length 1812;
Best Local Similarity 56.4%; Pred. No. 2.6e+02;
RESULT 1171
ID ABL52758 standard; DNA; 1854 BP.
DE Plant defence gene promoter region P1075.
PN WO200212483-A1.
PD 14-FEB-2002.
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
PA (QUEE-) STATE QUEENSLAND DEPT PRIMARY IND.
PA (UYOU) UNIV QUEENSLAND.
PA (SUGA-) BUREAU SUGAR EXPERIMENT STATIONS.
PA (GRAI-) GRAINS RES & DEV CORP.
Query Match 4.0%; Score 30.6; DB 6; Length 1854;
Best Local Similarity 48.1%; Pred. No. 2.6e+02;
RESULT 1172
ID ABV25351 standard; cDNA; 2206 BP.
DE Human prostate expression marker cDNA 25342.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.6; DB 5; Length 2206;
Best Local Similarity 68.9%; Pred. No. 2.9e+02;
RESULT 1173
ID ACA36675 standard; DNA; 2463 BP.
DE Prokaryotic essential gene #18332.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.0%; Score 30.6; DB 8; Length 2463;
Best Local Similarity 53.8%; Pred. No. 3e+02;
RESULT 1174
ID AAA70144 standard; DNA; 2874 BP.
DE Plasmodium falciparum chromosome 2 related DNA sequence SEQ ID NO:277.
PN WO200025728-A2.
PD 11-MAY-2000.
PA (HOFF/) HOFFMAN S.
PA (CARU/) CARUCCI D.
PA (GARD/) GARDNER M.
PA (VENT/) VENTER J C.
Query Match 4.0%; Score 30.6; DB 3; Length 2874;
Best Local Similarity 48.1%; Pred. No. 3.2e+02;
RESULT 1175
ID AAH18524 standard; cDNA; 2881 BP.
DE Human cDNA sequence SEQ ID NO:18667.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 4.0%; Score 30.6; DB 4; Length 2881;
Best Local Similarity 48.9%; Pred. No. 3.2e+02;
RESULT 1176
ID AAQ29186 standard; cDNA; 2981 BP.
DE cDNA encoding Plasmodium SERA gene.
PN WO9216616-A1.
PD 01-OCT-1992.
PA (VIRO-) VIROGENETICS CORP.
Query Match 4.0%; Score 30.6; DB 2; Length 2981;
Best Local Similarity 48.1%; Pred. No. 3.3e+02;
RESULT 1177
ID AAQ67867 standard; DNA; 2981 BP.
DE p126.15 SERA cDNA insert.
PN WO9416716-A1.
PD 04-AUG-1994.
PA (VIRO-) VIROGENETICS CORP.
Query Match 4.0%; Score 30.6; DB 2; Length 2981;

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Best Local Similarity 48.1%; Pred. No. 3.3e+02;
RESULT 1178
ID AAQ80907 standard; cDNA; 2981 BP.
DE Plasmodium falciparum SERA gene cDNA.
PN WO9428930-A1.
PD 22-DEC-1994.
PA (VIRO-) VIROGENETICS CORP.
Query Match 4.0%; Score 30.6; DB 2; Length 2981;
Best Local Similarity 48.1%; Pred. No. 3.3e+02;
RESULT 1179
ID AAQ08451 standard; cDNA; 2981 BP.
DE Plasmodium falciparum SERA p126.15 encoding cDNA.
PN US942235-A.
PD 24-AUG-1999.
PA (HEAL-) HEALTH RES INC.
Query Match 4.0%; Score 30.6; DB 2; Length 2981;
Best Local Similarity 48.1%; Pred. No. 3.3e+02;
RESULT 1180
ID ABK15041 standard; cDNA; 3107 BP.
DE Plasmodium cDNA encoding serine repeat antigen, SERA.
PN US6333406-B1.
PD 25-DEC-2001.
PA (INSE/) INSELBURG J W.
PA (BZIK/) BZIK D J.
PA (HORI/) HORII T.
PA (SUGI/) SUGIYAMA T.
Query Match 4.0%; Score 30.6; DB 6; Length 3107;
Best Local Similarity 48.1%; Pred. No. 3.4e+02;
RESULT 1181
ID ABL61065 standard; cDNA; 3851 BP.
DE Proline-enriched gamma-carboxyl glutamate-protein 194.05 encoding cDNA.
PN CN131106-A.
PD 16-JAN-2002.
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
Query Match 4.0%; Score 30.6; DB 6; Length 3851;
Best Local Similarity 48.9%; Pred. No. 3.7e+02;
RESULT 1182
ID AAN81157 standard; DNA; 3975 BP.
DE Malaria-specific gene encoding 140kD antigen.
PN EP283882-A.
PD 28-SEP-1988.
PA (BEHW ) BEHRINGWERKE AG.
Query Match 4.0%; Score 30.6; DB 1; Length 3975;
Best Local Similarity 48.1%; Pred. No. 3.8e+02;
RESULT 1183
ID AAQ22999 standard; DNA; 3975 BP.
DE SERP gene.
PN EP474891-A.
PD 18-MAR-1992.
PA (BEHW ) BEHRINGWERKE AG.
Query Match 4.0%; Score 30.6; DB 2; Length 3975;
Best Local Similarity 48.1%; Pred. No. 3.8e+02;
RESULT 1184
ID ADQ23570 standard; DNA; 4944 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6390.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 4.0%; Score 30.6; DB 12; Length 4944;
Best Local Similarity 58.1%; Pred. No. 4.2e+02;
RESULT 1185
ID AAQ03568 standard; DNA; 6124 BP.
DE Sequence encoding the SERA protein of plasmodium.
PN WO9001549-A.
PD 22-FEB-1990.
PA (DART-) DARTMOUTH COLLEGE.
Query Match 4.0%; Score 30.6; DB 2; Length 6124;
Best Local Similarity 48.1%; Pred. No. 4.6e+02;
RESULT 1186
ID ABK15042 standard; DNA; 6124 BP.
DE plasmodium gene for serine repeat antigen, SERA.
PN US6333406-B1.
PD 25-DEC-2001.
PA (INSE/) INSELBURG J W.
PA (BZIK/) BZIK D J.
PA (HORI/) HORII T.
PA (SUGI/) SUGIYAMA T.
Query Match 4.0%; Score 30.6; DB 6; Length 6124;
Best Local Similarity 48.1%; Pred. No. 4.6e+02;
RESULT 1187
ID AAT18767 standard; cDNA; 6578 BP.
DE RSV RNA-dependent RNA-polymerase L cDNA.
PN WO9610400-A1.
PD 11-APR-1996.
PA (UABR-) UAB RES FOUND.
Query Match 4.0%; Score 30.6; DB 2; Length 6578;
Best Local Similarity 49.7%; Pred. No. 4.8e+02;
RESULT 1188
ID AAV48171 standard; cDNA; 6578 BP.
DE Respiratory syncytial virus RNA dependent RNA polymerase.
PN US5789229-A.
PD 04-AUG-1998.
PA (UABR-) UAB RES FOUND.
Query Match 4.0%; Score 30.6; DB 2; Length 6578;
Best Local Similarity 49.7%; Pred. No. 4.8e+02;
RESULT 1189
ID AAI66080 standard; DNA; 7523 BP.
DE Listeria monocytogenes ClpC ATPase (mec) gene (GenBank: U40604).
PN WO200170929-A2.
PD 27-SEP-2001.
PA (ARCH-) ARCH DEV CORP.
Query Match 4.0%; Score 30.6; DB 4; Length 7523;
Best Local Similarity 53.8%; Pred. No. 5.1e+02;
RESULT 1190
ID ABL32077 standard; DNA; 7728 BP.
DE Human immune system associated gene SEQ ID NO: 50.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.0%; Score 30.6; DB 6; Length 7728;
Best Local Similarity 47.6%; Pred. No. 5.1e+02;
RESULT 1191
ID AAD28367 standard; DNA; 7728 BP.
DE Human chemically treated genomic DNA #8.
PN WO200202809-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.0%; Score 30.6; DB 6; Length 7728;
Best Local Similarity 47.6%; Pred. No. 5.1e+02;
RESULT 1192
ID ABL19348 standard; DNA; 8124 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 9517.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Query Match 4.0%; Score 30.6; DB 4; Length 8124;
Best Local Similarity 56.4%; Pred. No. 5.3e+02;
RESULT 1193
ID ABL33544 standard; DNA; 10328 BP.
DE Human immune system associated gene SEQ ID NO: 1517.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.0%; Score 30.6; DB 6; Length 10328;
Best Local Similarity 49.1%; Pred. No. 5.9e+02;
RESULT 1194
ID AAS45410 standard; DNA; 11036 BP.
DE Chemically pretreated genomic DNA associated with cell cycle #58.
PN WO200168911-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.0%; Score 30.6; DB 4; Length 11036;
Best Local Similarity 68.9%; Pred. No. 6.1e+02;
RESULT 1195
ID ABK28263 standard; DNA; 11036 BP.
DE DNA transcription associated genomic DNA #69.
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PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.0%; Score 30.6; DB 6; Length 11036;
Best Local Similarity 68.9%; Pred. No. 6.1e+02;
RESULT 1196
ID AAL36231 standard; DNA; 13819 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 2596.
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.0%; Score 30.6; DB 4; Length 13819;
Best Local Similarity 65.2%; Pred. No. 6.8e+02;
RESULT 1197
ID ABX59219 standard; cDNA; 13819 BP.
DE cDNA encoding novel human musculoskeletal system antigen #1563.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 4.0%; Score 30.6; DB 8; Length 13819;
Best Local Similarity 65.2%; Pred. No. 6.8e+02;
RESULT 1198
ID ADJ29969 standard; DNA; 13819 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 2596.
PN US2004009488-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.0%; Score 30.6; DB 12; Length 13819;
Best Local Similarity 65.2%; Pred. No. 6.8e+02;
RESULT 1199
ID AAL36230 standard; DNA; 13821 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 2595.
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.0%; Score 30.6; DB 4; Length 13821;
Best Local Similarity 65.2%; Pred. No. 6.8e+02;
RESULT 1200
ID ABX59218 standard; cDNA; 13821 BP.
DE cDNA encoding novel human musculoskeletal system antigen #1562.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 4.0%; Score 30.6; DB 8; Length 13821;
Best Local Similarity 65.2%; Pred. No. 6.8e+02;
RESULT 1201
ID ADJ29968 standard; DNA; 13821 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 2595.
PN US2004009488-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.0%; Score 30.6; DB 12; Length 13821;
Best Local Similarity 65.2%; Pred. No. 6.8e+02;
RESULT 1202
ID AAX59703 standard; DNA; 15210 BP.
DE Polynucleotide sequence of RSV strain A2.
PN WO9922742-A1.
PD 14-MAY-1999.
PA (CLEV-) CLEVELAND CLINIC FOUND.
PA (USSH) US NAT INST OF HEALTH.
Query Match 4.0%; Score 30.6; DB 2; Length 15210;
Best Local Similarity 49.7%; Pred. No. 7.1e+02;
RESULT 1203
ID AAT78440 standard; DNA; 15222 BP.
DE Human respiratory syncytial virus strain A2.
PN WO9729757-A1.
PD 21-AUG-1997.
PA (CLEV-) CLEVELAND CLINIC FOUND.
PA (USSH) US NAT INST OF HEALTH.

Query Match 4.0%; Score 30.6; DB 2; Length 15222;
Best Local Similarity 49.7%; Pred. No. 7.1e+02;
RESULT 1204
ID AAT63430 standard; DNA; 15223 BP.
DE Respiratory syncytial virus anti-genome.
PN WO9712032-A1.
PD 03-APR-1997.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 4.0%; Score 30.6; DB 2; Length 15223;
Best Local Similarity 49.7%; Pred. No. 7.1e+02;
RESULT 1205
ID AAV17553 standard; cDNA; 15223 BP.
DE Respiratory syncytial virus antigenome.
PN WO9802530-A1.
PD 22-JAN-1998.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 4.0%; Score 30.6; DB 2; Length 15223;
Best Local Similarity 49.7%; Pred. No. 7.1e+02;
RESULT 1206
ID AAA88743 standard; cDNA; 15223 BP.
DE Respiratory syncytial virus D46 5'-3' positive sense sequence.
PN WO200061611-A2.
PD 19-OCT-2000.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 4.0%; Score 30.6; DB 3; Length 15223;
Best Local Similarity 49.7%; Pred. No. 7.1e+02;
RESULT 1207
ID ABL32050 standard; DNA; 16545 BP.
DE Human immune system associated gene SEQ ID NO: 23.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.0%; Score 30.6; DB 6; Length 16545;
Best Local Similarity 55.0%; Pred. No. 7.4e+02;
RESULT 1208
ID ABK31171 standard; DNA; 17293 BP.
DE Signal transduction associated gene modified complementary DNA #7.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.0%; Score 30.6; DB 6; Length 17293;
Best Local Similarity 49.1%; Pred. No. 7.5e+02;
RESULT 1209
ID ABL70126 standard; DNA; 17293 BP.
DE Chemically treated cell signalling DNA sequence complementary to#8.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.0%; Score 30.6; DB 6; Length 17293;
Best Local Similarity 49.1%; Pred. No. 7.5e+02;
RESULT 1210
ID AAS61058 standard; DNA; 17293 BP.
DE Human gene regulation-associated gene oligonucleotide #13.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.0%; Score 30.6; DB 6; Length 17293;
Best Local Similarity 49.1%; Pred. No. 7.5e+02;
RESULT 1211
ID AAK71667 standard; DNA; 17379 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:26479.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.0%; Score 30.6; DB 4; Length 17379;
Best Local Similarity 55.0%; Pred. No. 7.5e+02;
RESULT 1212
ID AAS28427 standard; DNA; 17379 BP.
DE Genomic sequence #267 encoding for novel human respiratory antigen.
PN WO200155448-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.0%; Score 30.6; DB 4; Length 17379;

Best Local Similarity 55.0%; Pred. No. 7.5e+02;
RESULT 1213
ID ADG41623 standard; DNA; 17379 BP.
DE Human respiratory system associated genomic DNA seq id 861.
PN US2003215893-A1.
PD 20-NOV-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.0%; Score 30.6; DB 10; Length 17379;
Best Local Similarity 55.0%; Pred. No. 7.5e+02;
RESULT 1214
ID ABL16042 standard; cDNA; 22253 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 42608.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.0%; Score 30.6; DB 4; Length 22253;
Best Local Similarity 48.6%; Pred. No. 8.4e+02;
RESULT 1215
ID ADC20666 standard; DNA; 51961 BP.
DE Human secreted protein-related DNA sequence #84.
PN WO200292787-A2.
PD 21-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.0%; Score 30.6; DB 10; Length 51961;
Best Local Similarity 52.8%; Pred. No. 1.2e+03;
RESULT 1216
ID ABT16905 standard; DNA; 51961 BP.
DE Human secreted protein-related DNA sequence - SEQ ID No 259.
PN WO200277188-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.0%; Score 30.6; DB 10; Length 51961;
Best Local Similarity 52.8%; Pred. No. 1.2e+03;
RESULT 1217
ID ABZ67488 standard; DNA; 51961 BP.
DE Human secreted protein encoding genomic DNA SEQ ID NO 1011.
PN WO200277186-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.0%; Score 30.6; DB 10; Length 51961;
Best Local Similarity 52.8%; Pred. No. 1.2e+03;
RESULT 1218
Query Match 4.0%; Score 30.6; DB 2; Length 110000;
Best Local Similarity 51.9%; Pred. No. 1.8e+03;
RESULT 1219
ID AAF22303 standard; DNA; 611590 BP.
DE Arabidopsis thaliana chromosome 2 centromere.
PN WO200055325-A2.
PD 21-SEP-2000.
PA (UYCH-) UNIV CHICAGO.
Query Match 4.0%; Score 30.6; DB 3; Length 110000;
Best Local Similarity 51.1%; Pred. No. 1.8e+03;
RESULT 1220
Query Match 4.0%; Score 30.6; DB 6; Length 110000;
Best Local Similarity 50.3%; Pred. No. 1.8e+03;
RESULT 1221
Query Match 4.0%; Score 30.6; DB 6; Length 110000;
Best Local Similarity 53.8%; Pred. No. 1.8e+03;
RESULT 1222
ID AAD54634 standard; DNA; 142519 BP.
DE Human chromodomain helicase DNA binding protein (CHD) encoding DNA #9.
PN WO200298899-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 4.0%; Score 30.6; DB 10; Length 142519;
Best Local Similarity 46.2%; Pred. No. 2e+03;
RESULT 1223
ID ADH30232 standard; DNA; 161671 BP.
DE Human PLOD2 DNA.
PN US2003124535-A1.
PD 03-JUL-2003.
PA (VITI-) VITIVITY INC.
Query Match 4.0%; Score 30.6; DB 12; Length 161671;

Best Local Similarity 46.2%; Pred. No. 2.1e+03;
RESULT 1224
ID ABS55200 standard; DNA; 341511 BP.
DE Genomic DNA encoding human transporter protein.
Query Match 4.0%; Score 30.6; DB 6; Length 341511;
Best Local Similarity 50.3%; Pred. No. 2.7e+03;
RESULT 1225
ID ADQ05495 standard; DNA; 280 BP.
DE Soybean zinc finger transcription factor seqid 2341.
PN US2004123339-A1.
PD 24-JUN-2004.
PA (CONN/) CONNER T W.
PA (HECK/) HECK G R.
PA (LIUJ/) LIU J.
Query Match 4.0%; Score 30.4; DB 12; Length 280;
Best Local Similarity 53.3%; Pred. No. 1.3e+02;
RESULT 1226
ID ABL62993 standard; DNA; 308 BP.
DE Breast cancer related gene sequence SEQ ID NO:1330.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 4.0%; Score 30.4; DB 6; Length 308;
Best Local Similarity 45.4%; Pred. No. 1.3e+02;
RESULT 1227
ID ABL62809 standard; DNA; 308 BP.
DE Breast cancer related gene sequence SEQ ID NO:1146.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 4.0%; Score 30.4; DB 6; Length 308;
Best Local Similarity 45.4%; Pred. No. 1.3e+02;
RESULT 1228
ID ABL62070 standard; DNA; 308 BP.
DE Colon adenocarcinoma related gene sequence SEQ ID NO:407.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 4.0%; Score 30.4; DB 6; Length 308;
Best Local Similarity 45.4%; Pred. No. 1.3e+02;
RESULT 1229
ID ABV02543 standard; cDNA; 438 BP.
DE Human prostate expression marker cDNA 2534.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.4; DB 5; Length 438;
Best Local Similarity 52.5%; Pred. No. 1.5e+02;
RESULT 1230
ID ACH72411 standard; DNA; 600 BP.
DE Human genome derived single exon probe #5606.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match 4.0%; Score 30.4; DB 12; Length 600;
Best Local Similarity 55.8%; Pred. No. 1.8e+02;
RESULT 1231
ID ABV51715 standard; cDNA; 606 BP.
DE Human prostate expression marker cDNA 51706.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.4; DB 5; Length 606;
Best Local Similarity 63.9%; Pred. No. 1.8e+02;
RESULT 1232
ID ABN62149 standard; cDNA; 618 BP.
DE Human cancer related polynucleotide SEQ ID NO 2116.
PN WO200214500-A2.
PD 21-FEB-2002.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.

Query Match 4.0%; Score 30.4; DB 6; Length 618;
Best Local Similarity 53.3%; Pred. No. 1.8e+02;
RESULT 1233
ID AAI95397 standard; cDNA; 756 BP.
DE Human neuroblastoma expressed polynucleotide SEQ ID NO 1472.
PN WO200166719-A1.
PD 13-SEP-2001.
PA (CHIB-) CHIBA PREFECTURE.
PA (HISM) HISAMITSU PHARM CO LTD.
Query Match 4.0%; Score 30.4; DB 4; Length 756;
Best Local Similarity 63.2%; Pred. No. 2e+02;
RESULT 1234
ID AAI95724 standard; cDNA; 783 BP.
DE Human neuroblastoma expressed polynucleotide SEQ ID NO 1799.
PN WO200166719-A1.
PD 13-SEP-2001.
PA (CHIB-) CHIBA PREFECTURE.
PA (HISM) HISAMITSU PHARM CO LTD.
Query Match 4.0%; Score 30.4; DB 4; Length 783;
Best Local Similarity 48.8%; Pred. No. 2e+02;
RESULT 1235
ID AAH08126 standard; cDNA; 792 BP.
DE Human cDNA clone (5'-primer) SEQ ID NO:4961.
PN EPI074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 4.0%; Score 30.4; DB 4; Length 792;
Best Local Similarity 63.9%; Pred. No. 2e+02;
RESULT 1236
ID ADO62586 standard; DNA; 823 BP.
DE Transcription factor G1779 orthologous sequence, SEQ ID 1053.
PN WO2004031349-A2.
PD 15-APR-2004.
PA (MENDEL-) MENDEL BIOTECHNOLOGY INC.
Query Match 4.0%; Score 30.4; DB 12; Length 823;
Best Local Similarity 53.3%; Pred. No. 2.1e+02;
RESULT 1237
ID AAS71828 standard; cDNA; 981 BP.
DE DNA encoding novel human diagnostic protein #7632.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.0%; Score 30.4; DB 5; Length 981;
Best Local Similarity 54.5%; Pred. No. 2.3e+02;
RESULT 1238
ID ACF72474 standard; DNA; 1062 BP.
DE Staphylococcus aureus DNA #154.
PN WO200294868-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
Query Match 4.0%; Score 30.4; DB 8; Length 1062;
Best Local Similarity 50.0%; Pred. No. 2.3e+02;
RESULT 1239
ID AAS55149 standard; DNA; 1065 BP.
DE Staphylococcus aureus DNA for cellular proliferation protein #1461.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.0%; Score 30.4; DB 4; Length 1065;
Best Local Similarity 50.0%; Pred. No. 2.3e+02;
RESULT 1240
ID AAX83358 standard; cDNA; 1205 BP.
DE Breast cancer tumour specific clone #112.
PN WO9725426-A2.
PD 17-JUL-1997.
PA (CORI-) CORIXA CORP.
Query Match 4.0%; Score 30.4; DB 2; Length 1205;
Best Local Similarity 45.4%; Pred. No. 2.5e+02;
RESULT 1241
ID AAC80881 standard; cDNA; 1205 BP.
DE Human breast tumour-specific cDNA SEQ ID NO: 169.
PN WO200061753-A2.
PD 19-OCT-2000.

PA (CORI-) CORIXA CORP.
Query Match 4.0%; Score 30.4; DB 3; Length 1205;
Best Local Similarity 45.4%; Pred. No. 2.5e+02;
RESULT 1242
ID AAS99727 standard; cDNA; 1205 BP.
DE Breast tumour-specific DNA #102.
PN WO200190152-A2.
PD 29-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 4.0%; Score 30.4; DB 6; Length 1205;
Best Local Similarity 45.4%; Pred. No. 2.5e+02;
RESULT 1243
ID ABK46771 standard; cDNA; 1205 BP.
DE Human breast tumour-specific cDNA #89.
PN US6344550-B1.
PD 05-FEB-2002.
PA (CORI-) CORIXA CORP.
Query Match 4.0%; Score 30.4; DB 6; Length 1205;
Best Local Similarity 45.4%; Pred. No. 2.5e+02;
RESULT 1244
ID AAK72633 standard; DNA; 1223 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27445.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.0%; Score 30.4; DB 4; Length 1223;
Best Local Similarity 53.3%; Pred. No. 2.5e+02;
RESULT 1245
ID AAK72634 standard; DNA; 1224 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27446.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.0%; Score 30.4; DB 4; Length 1224;
Best Local Similarity 53.3%; Pred. No. 2.5e+02;
RESULT 1246
ID AAV68898 standard; DNA; 1265 BP.
DE DNA molecule encoding a breast tumour specific polypeptide #90.
PN WO9845328-A2.
PD 15-OCT-1998.
PA (CORI-) CORIXA CORP.
Query Match 4.0%; Score 30.4; DB 2; Length 1265;
Best Local Similarity 45.4%; Pred. No. 2.5e+02;
RESULT 1247
ID ADA11248 standard; cDNA; 1265 BP.
DE Human breast cancer specific cDNA #104.
PN US2002165371-A1.
PD 07-NOV-2002.
PA (FRUD/) FRUDAKIS T N.
PA (REED/) REED S G.
PA (SMIT/) SMITH J M.
PA (MISH/) MISHNER L E.
PA (DILL/) DILLON D C.
PA (RETT/) RETTER M W.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY V A W.
PA (HARL/) HARLOCKER S L.
PA (DAYC/) DAY C H.
PA (LISX/) LI S X.
PA (DENG/) DENG T.
Query Match 4.0%; Score 30.4; DB 8; Length 1265;
Best Local Similarity 45.4%; Pred. No. 2.5e+02;
RESULT 1248
ID ADC15221 standard; cDNA; 1265 BP.
DE Human breast tumour protein cDNA, SEQ ID 169.
PN WO2003013431-A2.
PD 20-FEB-2003.
PA (CORI-) CORIXA CORP.
Query Match 4.0%; Score 30.4; DB 10; Length 1265;
Best Local Similarity 45.4%; Pred. No. 2.5e+02;
RESULT 1249
ID ADM01599 standard; cDNA; 2118 BP.
DE Human cDNA of the invention SEQ ID NO:284.

PN EPI347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 4.0%; Score 30.4; DB 11; Length 2118;
Best Local Similarity 53.3%; Pred. No. 3.2e+02;
RESULT 1250
ID AAC99030 standard; cDNA; 2217 BP.
DE Human pancreatic cancer antigen nucleotide sequence SEQ ID NO:258.
PN WO200055320-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.0%; Score 30.4; DB 3; Length 2217;
Best Local Similarity 45.4%; Pred. No. 3.3e+02;
RESULT 1251
ID ACC72667 standard; cDNA; 2373 BP.
DE Human cancer-related protein encoding cDNA SEQ ID NO:6.
PN WO2003025138-A2.
PD 27-MAR-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 4.0%; Score 30.4; DB 10; Length 2373;
Best Local Similarity 45.4%; Pred. No. 3.4e+02;
RESULT 1252
ID ADQ25329 standard; DNA; 2373 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 8149.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 4.0%; Score 30.4; DB 12; Length 2373;
Best Local Similarity 45.4%; Pred. No. 3.4e+02;
RESULT 1253
ID AAH72845 standard; cDNA; 2950 BP.
DE Human cervical cancer marker nucleic acid 4119.
PN WO200142467-A2.
PD 14-JUN-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.4; DB 4; Length 2950;
Best Local Similarity 45.4%; Pred. No. 3.8e+02;
RESULT 1254
ID AAH72686 standard; cDNA; 2950 BP.
DE Human cervical cancer marker nucleic acid 3960.
PN WO200142467-A2.
PD 14-JUN-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.4; DB 4; Length 2950;
Best Local Similarity 45.4%; Pred. No. 3.8e+02;
RESULT 1255
ID ADL46049 standard; DNA; 2987 BP.
DE Human ovarian cancer DNA marker #19939.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.0%; Score 30.4; DB 5; Length 2987;
Best Local Similarity 45.4%; Pred. No. 3.8e+02;
RESULT 1256
ID ADI05016 standard; DNA; 3204 BP.
DE aadA/BADH expression cassette.
PN WO2004005480-A2.
PD 15-JAN-2004.
PA (UYFL-) UNIV CENT FLORIDA.
Query Match 4.0%; Score 30.4; DB 12; Length 3204;
Best Local Similarity 53.3%; Pred. No. 3.9e+02;
RESULT 1257
ID ADI05017 standard; DNA; 3300 BP.
DE gfp/BADH expression cassette.
PN WO2004005480-A2.
PD 15-JAN-2004.
PA (UYFL-) UNIV CENT FLORIDA.
Query Match 4.0%; Score 30.4; DB 12; Length 3300;
Best Local Similarity 53.3%; Pred. No. 4e+02;
RESULT 1258
ID AAA70099 standard; DNA; 3579 BP.
DE Plasmodium falciparum chromosome 2 related DNA sequence SEQ ID NO:232.
PN WO200025728-A2.

PD 11-MAY-2000.
PA (HOFF/) HOFFMAN S.
PA (CARU/) CARUCCI D.
PA (GARD/) GARDNER M.
PA (VENT/) VENTER J C.
Query Match 4.0%; Score 30.4; DB 3; Length 3579;
Best Local Similarity 55.8%; Pred. No. 4.1e+02;
RESULT 1259
ID ABT17682 standard; DNA; 4208 BP.
DE Aspergillus fumigatus essential gene #40.
PN WO200286090-A2.
PD 31-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.0%; Score 30.4; DB 8; Length 4208;
Best Local Similarity 61.2%; Pred. No. 4.5e+02;
RESULT 1260
ID ABT19496 standard; DNA; 4529 BP.
DE Aspergillus fumigatus essential gene #1854.
PN WO200286090-A2.
PD 31-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.0%; Score 30.4; DB 8; Length 4529;
Best Local Similarity 61.2%; Pred. No. 4.6e+02;
RESULT 1261
ID AAS71832 standard; cDNA; 4651 BP.
DE DNA encoding novel human diagnostic protein #7636.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.0%; Score 30.4; DB 5; Length 4651;
Best Local Similarity 54.5%; Pred. No. 4.7e+02;
RESULT 1262
ID ABL30444 standard; DNA; 5223 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 42805.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.0%; Score 30.4; DB 4; Length 5223;
Best Local Similarity 47.0%; Pred. No. 4.9e+02;
RESULT 1263
ID ABK33934 standard; DNA; 5310 BP.
DE Human DNA for staging of Astrocytomas #9.
PN WO200202808-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.0%; Score 30.4; DB 6; Length 5310;
Best Local Similarity 48.8%; Pred. No. 5e+02;
RESULT 1264
ID ADA20346 standard; DNA; 5310 BP.
DE Prostate tumour related genomic DNA sample #6.
PN WO2002103042-A2.
PD 27-DEC-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.0%; Score 30.4; DB 8; Length 5310;
Best Local Similarity 48.8%; Pred. No. 5e+02;
RESULT 1265
ID ADA84153 standard; DNA; 5310 BP.
DE Human renal/prostate carcinoma associated DNA SEQ ID NO:11.
PN WO2002103041-A2.
PD 27-DEC-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.0%; Score 30.4; DB 8; Length 5310;
Best Local Similarity 48.8%; Pred. No. 5e+02;
RESULT 1266
ID ADE84083 standard; DNA; 5310 BP.
DE Human lymphoid cell proliferative disorder gene derived DNA #19.
PN WO2003044226-A2.
PD 30-MAY-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.0%; Score 30.4; DB 10; Length 5310;
Best Local Similarity 48.8%; Pred. No. 5e+02;
RESULT 1267
ID ABL32132 standard; DNA; 5421 BP.

DE Human immune system associated gene SEQ ID NO: 105.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.0%; Score 30.4; DB 6; Length 5421;
Best Local Similarity 71.4%; Pred. No. 5e+02;
RESULT 1268
ID AAV74613 standard; DNA; 7159 BP.
DE Staphylococcus aureus contig SEQ ID #302.
PN EP786519-A2.
PD 30-JUL-1997.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.0%; Score 30.4; DB 2; Length 7159;
Best Local Similarity 50.0%; Pred. No. 5.7e+02;
RESULT 1269
ID ABL32896 standard; DNA; 8131 BP.
DE Human immune system associated gene SEQ ID NO: 869.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.0%; Score 30.4; DB 6; Length 8131;
Best Local Similarity 55.8%; Pred. No. 6.1e+02;
RESULT 1270
ID AAS63326 standard; DNA; 8131 BP.
DE Chemically pretreated metabolism associated gene #21.
PN WO200176451-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.0%; Score 30.4; DB 6; Length 8131;
Best Local Similarity 55.8%; Pred. No. 6.1e+02;
RESULT 1271
ID ABK31277 standard; DNA; 9087 BP.
DE Signal transduction associated gene modified complementary DNA #60.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.0%; Score 30.4; DB 6; Length 9087;
Best Local Similarity 49.4%; Pred. No. 6.4e+02;
RESULT 1272
ID ABL70238 standard; DNA; 9087 BP.
DE Chemically treated cell signalling DNA sequence complementary to #64.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.0%; Score 30.4; DB 6; Length 9087;
Best Local Similarity 49.4%; Pred. No. 6.4e+02;
RESULT 1273
ID AAS61181 standard; DNA; 9087 BP.
DE Human gene regulation-associated gene oligonucleotide #136.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.0%; Score 30.4; DB 6; Length 9087;
Best Local Similarity 49.4%; Pred. No. 6.4e+02;
RESULT 1274
ID ABL04304 standard; cDNA; 13359 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 7394.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.0%; Score 30.4; DB 4; Length 13359;
Best Local Similarity 47.4%; Pred. No. 7.6e+02;
RESULT 1275
ID ABL32466 standard; DNA; 15373 BP.
DE Human immune system associated gene SEQ ID NO: 439.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.0%; Score 30.4; DB 6; Length 15373;
Best Local Similarity 47.4%; Pred. No. 8.2e+02;
RESULT 1276
ID ABL32185 standard; DNA; 15387 BP.
DE Human immune system associated gene SEQ ID NO: 158.

PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.0%; Score 30.4; DB 6; Length 15387;
Best Local Similarity 55.8%; Pred. No. 8.2e+02;
RESULT 1277
ID ABL33207 standard; DNA; 15767 BP.
DE Human immune system associated gene SEQ ID NO: 1180.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.0%; Score 30.4; DB 6; Length 15767;
Best Local Similarity 49.4%; Pred. No. 8.3e+02;
RESULT 1278
ID ABL34553 standard; DNA; 15767 BP.
DE Human metastasis associated gene SEQ ID NO: 106.
PN WO200177376-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.0%; Score 30.4; DB 6; Length 15767;
Best Local Similarity 49.4%; Pred. No. 8.3e+02;
RESULT 1279
ID ABL30408 standard; DNA; 15933 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 42697.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.0%; Score 30.4; DB 4; Length 15933;
Best Local Similarity 47.0%; Pred. No. 8.3e+02;
RESULT 1280
ID AAK73082 standard; DNA; 20188 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO: 27894.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.0%; Score 30.4; DB 4; Length 20188;
Best Local Similarity 55.8%; Pred. No. 9.3e+02;
RESULT 1281
ID AAK87550 standard; DNA; 20188 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO: 42362.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.0%; Score 30.4; DB 4; Length 20188;
Best Local Similarity 55.8%; Pred. No. 9.3e+02;
RESULT 1282
ID ABA07406 standard; DNA; 32249 BP.
DE Human pancreatic cancer related genomic DNA, SEQ ID NO: 725.
PN WO200155206-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.0%; Score 30.4; DB 4; Length 32249;
Best Local Similarity 55.8%; Pred. No. 1.2e+03;
RESULT 1283
ID AAK91137 standard; DNA; 32249 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 4713.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.0%; Score 30.4; DB 4; Length 32249;
Best Local Similarity 55.8%; Pred. No. 1.2e+03;
RESULT 1284
ID ABA20005 standard; DNA; 32249 BP.
DE Human nervous system related polynucleotide SEQ ID NO 12336.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.0%; Score 30.4; DB 5; Length 32249;
Best Local Similarity 55.8%; Pred. No. 1.2e+03;
RESULT 1285
ID AAK87551 standard; DNA; 50442 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO: 42363.
PN WO200157182-A2.

PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.0%; Score 30.4; DB 4; Length 50442;
Best Local Similarity 55.8%; Pred. No. 1.4e+03;
RESULT 1286
ID AAK73083 standard; DNA; 50442 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27895.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.0%; Score 30.4; DB 4; Length 50442;
Best Local Similarity 55.8%; Pred. No. 1.4e+03;
RESULT 1287
ID ADA02798 standard; DNA; 52754 BP.
DE Human TNFSF11 carcinoma associated gene, SEQ ID NO:1316.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 4.0%; Score 30.4; DB 9; Length 52754;
Best Local Similarity 46.0%; Pred. No. 1.4e+03;
RESULT 1288
ID ADB72536 standard; DNA; 52754 BP.
DE Human TNFSF11 gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 4.0%; Score 30.4; DB 10; Length 52754;
Best Local Similarity 46.0%; Pred. No. 1.4e+03;
RESULT 1289
ID ADC85278 standard; DNA; 52754 BP.
DE Human Tnfsf11 genomic sequence.
PN WO2003045230-A2.
PD 05-JUN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 4.0%; Score 30.4; DB 10; Length 52754;
Best Local Similarity 46.0%; Pred. No. 1.4e+03;
RESULT 1290
ID ADM74393 standard; DNA; 52754 BP.
DE Human carcinoma associated (CA) nucleic acid #31.
PN US2004072154-A1.
PD 15-APR-2004.
PA (MORR/) MORRIS D W.
PA (ENGE/) ENGELHARD E K.
Query Match 4.0%; Score 30.4; DB 12; Length 52754;
Best Local Similarity 46.0%; Pred. No. 1.4e+03;
RESULT 1291
Query Match 4.0%; Score 30.4; DB 2; Length 110000;
Best Local Similarity 45.2%; Pred. No. 2e+03;
RESULT 1292
ID ADF77343 standard; DNA; 1983043 BP.
DE Lactic acid bacteria Lactobacillus johnsonii Lal genomic DNA SEQ ID NO:1.
PN WO2003084989-A2.
PD 16-OCT-2003.
PA (NEST) SOC PROD NESTLE SA.
Query Match 4.0%; Score 30.4; DB 10; Length 110000;
Best Local Similarity 50.7%; Pred. No. 2e+03;
RESULT 1293
ID ADF13110 standard; DNA; 118067 BP.
DE Hypermethylation site in human breast cancer CpG island locus HBC-37.
PN US2003129602-A1.
PD 10-JUL-2003.
PA (HUAN/) HUANG T H.
Query Match 4.0%; Score 30.4; DB 12; Length 118067;
Best Local Similarity 47.4%; Pred. No. 2.1e+03;
RESULT 1294
ID ADI37256 standard; DNA; 118067 BP.
DE Hypermethylation in cancer (HBC) locus-37.
PN US6605432-B1.
PD 12-AUG-2003.
PA (UMOR) UNIV MISSOURI.
Query Match 4.0%; Score 30.4; DB 12; Length 118067;
Best Local Similarity 47.4%; Pred. No. 2.1e+03;
RESULT 1295

ID ADL08126 standard; DNA; 191395 BP.
DE Human gene associated with low HDL-C PAI2.
PN US2004043389-A1.
PD 04-MAR-2004.
PA (VITI-) VITIVITY INC.
Query Match 4.0%; Score 30.4; DB 12; Length 191395;
Best Local Similarity 50.0%; Pred. No. 2.5e+03;
RESULT 1296
ID AAC06534 standard; CDNA; 442 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 10609.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Query Match 3.9%; Score 30.2; DB 3; Length 442;
Best Local Similarity 50.4%; Pred. No. 1.8e+02;
RESULT 1297
ID ABV52363 standard; CDNA; 493 BP.
DE Human prostate expression marker CDNA 52354.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.9%; Score 30.2; DB 5; Length 493;
Best Local Similarity 56.6%; Pred. No. 1.9e+02;
RESULT 1298
ID ADQ18344 standard; DNA; 532 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1163.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 3.9%; Score 30.2; DB 12; Length 532;
Best Local Similarity 52.8%; Pred. No. 1.9e+02;
RESULT 1299
ID AAF68671 standard; CDNA; 572 BP.
DE Human lung tumour protein related nucleotide sequence SEQ ID NO:606.
PN WO200100828-A2.
PD 04-JAN-2001.
PA (CORI-) CORIXA CORP.
Query Match 3.9%; Score 30.2; DB 5; Length 572;
Best Local Similarity 47.9%; Pred. No. 2e+02;
RESULT 1300
ID ABK38582 standard; CDNA; 572 BP.
DE CDNA encoding clone #26264 of lung tumour protein.
PN WO200204514-A2.
PD 17-JAN-2002.
PA (CORI-) CORIXA CORP.
Query Match 3.9%; Score 30.2; DB 6; Length 572;
Best Local Similarity 47.9%; Pred. No. 2e+02;
RESULT 1301
ID ACA10911 standard; CDNA; 572 BP.
DE Human lung neuroendocrine carcinoma library MLN1 CDNA, SEQ ID 606.
PN US2002197669-A1.
PD 26-DEC-2002.
PA (BANG/) BANGUR C S.
PA (FANG/) FANGER G R.
PA (WANG/) WANG A.
PA (SWIT/) SWITZER A P.
PA (MCNE/) MCNEILL P D.
PA (CLAP/) CLAPPER J D.
Query Match 3.9%; Score 30.2; DB 8; Length 572;
Best Local Similarity 47.9%; Pred. No. 2e+02;
RESULT 1302
ID ABX99862 standard; CDNA; 572 BP.
DE Lung cancer therapy and diagnosis associated CDNA #589.
PN US2002172952-A1.
PD 21-NOV-2002.
PA (CORI-) CORIXA CORP.
Query Match 3.9%; Score 30.2; DB 8; Length 572;
Best Local Similarity 47.9%; Pred. No. 2e+02;
RESULT 1303
ID ADH46125 standard; CDNA; 572 BP.
DE Human lung tumour CDNA clone, SEQ ID No 606.
PN WO2003037267-A2.

PD 08-MAY-2003.
PA (CORI-) CORIXA CORP.
Query Match 3.9%; Score 30.2; DB 10; Length 572;
Best Local Similarity 47.9%; Pred. No. 2e+02;
RESULT 1304
ID ADE71877 standard; cDNA; 572 BP.
DE Human lung tumour protein cDNA #589.
PN US2003125245-A1.
PD 03-JUL-2003.
PA (WANG/) WANG T.
PA (BANG/) BANGUR C S.
Query Match 3.9%; Score 30.2; DB 12; Length 572;
Best Local Similarity 47.9%; Pred. No. 2e+02;
RESULT 1305
ID ABL90425 standard; cDNA; 637 BP.
DE Human polynucleotide SEQ ID NO 987.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.9%; Score 30.2; DB 6; Length 637;
Best Local Similarity 56.0%; Pred. No. 2.1e+02;
RESULT 1306
ID AAS55740 standard; DNA; 885 BP.
DE Streptococcus pneumoniae DNA for cellular proliferation protein #311.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 3.9%; Score 30.2; DB 4; Length 885;
Best Local Similarity 53.9%; Pred. No. 2.5e+02;
RESULT 1307
ID ACA50066 standard; DNA; 885 BP.
DE Prokaryotic essential gene #31723.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 3.9%; Score 30.2; DB 8; Length 885;
Best Local Similarity 53.9%; Pred. No. 2.5e+02;
RESULT 1308
ID ADC85778 standard; DNA; 985 BP.
DE Human GPCR gene SEQ ID NO:231.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 3.9%; Score 30.2; DB 10; Length 985;
Best Local Similarity 58.2%; Pred. No. 2.6e+02;
RESULT 1309
ID ADA30374 standard; DNA; 1014 BP.
DE DNA encoding Acinetobacter baumannii protein #1661.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 3.9%; Score 30.2; DB 9; Length 1014;
Best Local Similarity 56.6%; Pred. No. 2.6e+02;
RESULT 1310
ID ABQ76477 standard; cDNA; 1235 BP.
DE S. cerevisiae BAX-associated cDNA fragment SEQ ID 379.
PN WO200264766-A2.
PD 22-AUG-2002.
PA (JANC-) JANSSEN PHARM NV.
Query Match 3.9%; Score 30.2; DB 6; Length 1235;
Best Local Similarity 53.9%; Pred. No. 2.9e+02;
RESULT 1311
ID ADF41695 standard; DNA; 1353 BP.
DE Bacillus subtilis Csa coding sequence SEQ ID NO:17.
PN WO2003083125-A1.
PD 09-OCT-2003.
PA (GEMV-) GENENCOR INT INC.
Query Match 3.9%; Score 30.2; DB 10; Length 1353;
Best Local Similarity 60.2%; Pred. No. 3e+02;
RESULT 1312
ID ADO26017 standard; DNA; 1508 BP.
DE Cotton chalcone synthase (CHS) polynucleotide seqid 55.

PN WO2004046336-A2.
PD 03-JUN-2004.
PA (MONS-) MONSANTO TECHNOLOGY LLC.
Query Match 3.9%; Score 30.2; DB 12; Length 1508;
Best Local Similarity 58.2%; Pred. No. 3.2e+02;
RESULT 1313
ID ADA52483 standard; cDNA; 2624 BP.
DE Human coding sequence, SEQ ID 51.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 3.9%; Score 30.2; DB 10; Length 2624;
Best Local Similarity 51.9%; Pred. No. 4.1e+02;
RESULT 1314
ID AAH16320 standard; cDNA; 2687 BP.
DE Human cDNA sequence SEQ ID NO:15219.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 3.9%; Score 30.2; DB 4; Length 2687;
Best Local Similarity 52.7%; Pred. No. 4.2e+02;
RESULT 1315
ID ADI21920 standard; cDNA; 2848 BP.
DE Novel human protein cDNA #179.
PN WO2003025148-A2.
PD 27-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 3.9%; Score 30.2; DB 10; Length 2848;
Best Local Similarity 53.9%; Pred. No. 4.3e+02;
RESULT 1316
ID ADQ22541 standard; DNA; 2938 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5361.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 3.9%; Score 30.2; DB 12; Length 2938;
Best Local Similarity 48.0%; Pred. No. 4.3e+02;
RESULT 1317
ID ABQ79969 standard; cDNA; 3535 BP.
DE Human CD109 K15 variant protein encoding cDNA.
PN WO200270696-A2.
PD 12-SEP-2002.
PA (SCHU/) SCHUH A.
PA (SUTH/) SUTHERLAND R D.
Query Match 3.9%; Score 30.2; DB 6; Length 3535;
Best Local Similarity 48.0%; Pred. No. 4.7e+02;
RESULT 1318
ID ABQ79968 standard; cDNA; 3535 BP.
DE Human CD109 K15 protein encoding cDNA.
PN WO200270696-A2.
PD 12-SEP-2002.
PA (SCHU/) SCHUH A.
PA (SUTH/) SUTHERLAND R D.
Query Match 3.9%; Score 30.2; DB 6; Length 3535;
Best Local Similarity 48.0%; Pred. No. 4.7e+02;
RESULT 1319
ID AAD49436 standard; DNA; 4146 BP.
DE Human blood cell surface antigen, CD109 encoding DNA #1.
PN WO200285942-A2.
PD 31-OCT-2002.
PA (UYMC-) UNIV MCGILL.
Query Match 3.9%; Score 30.2; DB 8; Length 4146;
Best Local Similarity 48.0%; Pred. No. 5.1e+02;
RESULT 1320
ID AAD49437 standard; DNA; 4197 BP.
DE Human r150 DNA #2.
PN WO200285942-A2.
PD 31-OCT-2002.
PA (UYMC-) UNIV MCGILL.
Query Match 3.9%; Score 30.2; DB 8; Length 4197;
Best Local Similarity 48.0%; Pred. No. 5.1e+02;
RESULT 1321

ID AAA60199 standard; DNA; 4335 BP.
DE Hydrophobic domain protein cDNA HP02837 isolated from HT-1080 cells.
PN WO200029448-A2.
PD 25-MAY-2000.
PA (SAGA) SAGAMI CHEM RES CENT.
PA (PROT-) PROTEGENE INC.
Query Match 3.9%; Score 30.2; DB 3; Length 4335;
Best Local Similarity 48.0%; Pred. No. 5.2e+02;
RESULT 1322
ID AAL49816 standard; cDNA; 4335 BP.
DE Human platelet alloantigen Govb coding sequence.
PN WO200270738-A2.
PD 12-SEP-2002.
PA (SCHU/) SCHUH A.
Query Match 3.9%; Score 30.2; DB 6; Length 4335;
Best Local Similarity 48.0%; Pred. No. 5.2e+02;
RESULT 1323
ID AAL49815 standard; cDNA; 4335 BP.
DE Human platelet alloantigen Gova coding sequence.
PN WO200270738-A2.
PD 12-SEP-2002.
PA (SCHU/) SCHUH A.
Query Match 3.9%; Score 30.2; DB 6; Length 4335;
Best Local Similarity 48.0%; Pred. No. 5.2e+02;
RESULT 1324
ID AAD49434 standard; DNA; 4369 BP.
DE Human r150 gene #1.
PN WO200285942-A2.
PD 31-OCT-2002.
PA (UYMC-) UNIV MCGILL.
Query Match 3.9%; Score 30.2; DB 8; Length 4369;
Best Local Similarity 48.0%; Pred. No. 5.2e+02;
RESULT 1325
ID AAA62010 standard; DNA; 4473 BP.
DE Hydrophobic domain protein cDNA HP02837 isolated from HT-1080 cells.
PN WO200029448-A2.
PD 25-MAY-2000.
PA (SAGA) SAGAMI CHEM RES CENT.
PA (PROT-) PROTEGENE INC.
Query Match 3.9%; Score 30.2; DB 3; Length 4473;
Best Local Similarity 48.0%; Pred. No. 5.3e+02;
RESULT 1326
ID ABQ79964 standard; cDNA; 4761 BP.
DE Human CD109 K1 protein encoding cDNA.
PN WO200270696-A2.
PD 12-SEP-2002.
PA (SCHU/) SCHUH A.
PA (SUTH/) SUTHERLAND R D.
Query Match 3.9%; Score 30.2; DB 6; Length 4761;
Best Local Similarity 48.0%; Pred. No. 5.4e+02;
RESULT 1327
ID ABQ79965 standard; cDNA; 4761 BP.
DE Human CD109 K1 variant protein encoding cDNA.
PN WO200270696-A2.
PD 12-SEP-2002.
PA (SCHU/) SCHUH A.
PA (SUTH/) SUTHERLAND R D.
Query Match 3.9%; Score 30.2; DB 6; Length 4761;
Best Local Similarity 48.0%; Pred. No. 5.4e+02;
RESULT 1328
ID AAF44629 standard; cDNA; 4983 BP.
DE Novel protein kinase cDNA, SEQ ID NO: 8.
PN WO200073469-A2.
PD 07-DEC-2000.
PA (SUGE-) SUGEN INC.
Query Match 3.9%; Score 30.2; DB 4; Length 4983;
Best Local Similarity 55.1%; Pred. No. 5.5e+02;
RESULT 1329
ID ADI29327 standard; cDNA; 4983 BP.
DE Human MARK3-associated cDNA #6.
PN US2003232771-A1.
PD 18-DEC-2003.
PA (ISIS-) ISIS PHARM INC.

Query Match 3.9%; Score 30.2; DB 12; Length 4983;
Best Local Similarity 55.1%; Pred. No. 5.5e+02;
RESULT 1330
ID AAF30935 standard; cDNA; 5592 BP.
DE Spodoptera frugiperda Bt toxin receptor cDNA.
PN WO200136639-A2.
PD 25-MAY-2001.
PA (PION-) PIONEER HI-BRED INT INC.
Query Match 3.9%; Score 30.2; DB 4; Length 5592;
Best Local Similarity 52.0%; Pred. No. 5.9e+02;
RESULT 1331
ID AAD49440 standard; DNA; 5882 BP.
DE Human blood cell surface antigen, CD109 encoding DNA #2.
PN WO200285942-A2.
PD 31-OCT-2002.
PA (UYMC-) UNIV MCGILL.
Query Match 3.9%; Score 30.2; DB 8; Length 5882;
Best Local Similarity 48.0%; Pred. No. 6e+02;
RESULT 1332
ID AAD49435 standard; DNA; 5883 BP.
DE Human r150 DNA #1.
PN WO200285942-A2.
PD 31-OCT-2002.
PA (UYMC-) UNIV MCGILL.
Query Match 3.9%; Score 30.2; DB 8; Length 5883;
Best Local Similarity 48.0%; Pred. No. 6e+02;
RESULT 1333
ID ABQ79967 standard; cDNA; 5895 BP.
DE Human CD109 K1-H7 variant protein encoding cDNA.
PN WO200270696-A2.
PD 12-SEP-2002.
PA (SCHU/) SCHUH A.
PA (SUTH/) SUTHERLAND R D.
Query Match 3.9%; Score 30.2; DB 6; Length 5895;
Best Local Similarity 48.0%; Pred. No. 6e+02;
RESULT 1334
ID ABQ79966 standard; cDNA; 5895 BP.
DE Human CD109 K1-H7 protein encoding cDNA.
PN WO200270696-A2.
PD 12-SEP-2002.
PA (SCHU/) SCHUH A.
PA (SUTH/) SUTHERLAND R D.
Query Match 3.9%; Score 30.2; DB 6; Length 5895;
Best Local Similarity 48.0%; Pred. No. 6e+02;
RESULT 1335
ID AAS46515 standard; DNA; 5989 BP.
DE Tumour suppressor gene derived chemically modified sequence #237.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.9%; Score 30.2; DB 4; Length 5989;
Best Local Similarity 62.7%; Pred. No. 6e+02;
RESULT 1336
ID AAS45476 standard; DNA; 6203 BP.
DE Chemically pretreated genomic DNA associated with cell cycle #91.
PN WO200168911-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.9%; Score 30.2; DB 4; Length 6203;
Best Local Similarity 49.7%; Pred. No. 6.1e+02;
RESULT 1337
ID ABK28400 standard; DNA; 6203 BP.
DE DNA transcription associated complementary genomic DNA #137.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.9%; Score 30.2; DB 6; Length 6203;
Best Local Similarity 49.7%; Pred. No. 6.1e+02;
RESULT 1338
ID AAS93523 standard; cDNA; 7938 BP.
DE DNA encoding novel human diagnostic protein #29327.
PN WO200175067-A2.
PD 11-OCT-2001.

PA (HYSE-) HYSEQ INC.
Query Match 3.9%; Score 30.2; DB 5; Length 7938;
Best Local Similarity 50.3%; Pred. No. 6.9e+02;
RESULT 1339
ID ADB54262 standard; DNA; 8244 BP.
DE Pretreated genomic DNA region 186.
PN WO2003072821-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.9%; Score 30.2; DB 10; Length 8244;
Best Local Similarity 51.1%; Pred. No. 7e+02;
RESULT 1340
ID ABL70228 standard; DNA; 8897 BP.
DE Chemically treated cell signalling DNA sequence complementary to#59.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.9%; Score 30.2; DB 6; Length 8897;
Best Local Similarity 50.3%; Pred. No. 7.3e+02;
RESULT 1341
ID AAS76397 standard; cDNA; 9223 BP.
DE DNA encoding novel human diagnostic protein #12201.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 3.9%; Score 30.2; DB 5; Length 9223;
Best Local Similarity 50.3%; Pred. No. 7.4e+02;
RESULT 1342
ID AAS59531 standard; DNA; 9292 BP.
DE Propionibacterium acnes immunogenic protein encoding DNA #26.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 3.9%; Score 30.2; DB 4; Length 9292;
Best Local Similarity 62.7%; Pred. No. 7.4e+02;
RESULT 1343
ID ACF64460 standard; DNA; 9292 BP.
DE Propionibacterium acnes DNA contig sequence #26.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 3.9%; Score 30.2; DB 8; Length 9292;
Best Local Similarity 62.7%; Pred. No. 7.4e+02;
RESULT 1344
ID ABL32895 standard; DNA; 11729 BP.
DE Human immune system associated gene SEQ ID NO: 868.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.9%; Score 30.2; DB 6; Length 11729;
Best Local Similarity 48.0%; Pred. No. 8.3e+02;
RESULT 1345
ID ABK31474 standard; DNA; 12584 BP.
DE Signal transduction associated gene modified DNA #159.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.9%; Score 30.2; DB 6; Length 12584;
Best Local Similarity 49.7%; Pred. No. 8.6e+02;
RESULT 1346
ID ABL70445 standard; DNA; 12584 BP.
DE Chemically treated cell signalling DNA sequence#168.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.9%; Score 30.2; DB 6; Length 12584;
Best Local Similarity 49.7%; Pred. No. 8.6e+02;
RESULT 1347
ID AAS61398 standard; DNA; 12584 BP.
DE Human gene regulation-associated gene oligonucleotide #353.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.

Query Match 3.9%; Score 30.2; DB 6; Length 12584;
Best Local Similarity 49.7%; Pred. No. 8.6e+02;
RESULT 1348
ID ABN80146 standard; DNA; 14920 BP.
DE Human chemically modified disease associated gene SEQ ID NO 163.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.9%; Score 30.2; DB 6; Length 14920;
Best Local Similarity 48.5%; Pred. No. 9.3e+02;
RESULT 1349
ID ABK39964 standard; DNA; 15479 BP.
DE Human chemically pretreated gene sequence #23 strand 1.
PN WO200202806-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.9%; Score 30.2; DB 6; Length 15479;
Best Local Similarity 48.0%; Pred. No. 9.4e+02;
RESULT 1350
ID AAD19232 standard; DNA; 16545 BP.
DE Human CGI68 (or C595) receptor protein encoding DNA #2.
PN WO200179446-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 3.9%; Score 30.2; DB 5; Length 16545;
Best Local Similarity 51.9%; Pred. No. 9.7e+02;
RESULT 1351
ID ABK42737 standard; DNA; 20029 BP.
DE Genomic sequence #636 encoding novel human connective tissue polypeptide.
PN WO200155343-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.9%; Score 30.2; DB 4; Length 20029;
Best Local Similarity 50.3%; Pred. No. 1.1e+03;
RESULT 1352
ID ADB60893 standard; DNA; 20029 BP.
DE Connective tissue related genomic DNA #636.
PN US2003054375-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.9%; Score 30.2; DB 9; Length 20029;
Best Local Similarity 50.3%; Pred. No. 1.1e+03;
RESULT 1353
ID ABQ80553 standard; DNA; 47841 BP.
DE Human Canlon gene fragment #3.
PN WO200246404-A2.
PD 13-JUN-2002.
PA (GEST) GENSET.
Query Match 3.9%; Score 30.2; DB 6; Length 47841;
Best Local Similarity 46.8%; Pred. No. 1.6e+03;
RESULT 1354
ID AAZ10752 standard; DNA; 72604 BP.
DE Genomic sequence of the human HKNG1 gene.
PN WO9947535-A1.
PD 23-SEP-1999.
PA (MILL-) MILLENNIUM PHARM INC.
PA (REGC) UNIV CALIFORNIA.
Query Match 3.9%; Score 30.2; DB 2; Length 72604;
Best Local Similarity 55.1%; Pred. No. 1.9e+03;
RESULT 1355
ID ABK43231 standard; DNA; 72604 BP.
DE Human HKNG1 gene.
PN WO200210366-A2.
PD 07-FEB-2002.
PA (MILL-) MILLENNIUM PHARM INC.
PA (REGC) UNIV CALIFORNIA.
Query Match 3.9%; Score 30.2; DB 6; Length 72604;
Best Local Similarity 55.1%; Pred. No. 1.9e+03;
RESULT 1356
ID AAS61398 standard; DNA; 12584 BP.
DE Human gene regulation-associated gene oligonucleotide #353.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.

Best Local Similarity. 53.9%; Pred. No. 2.3e+03;
RESULT 1358
ID ABK94701 standard; DNA; 323 BP.
DE Neurodegenerative disease associated polynucleotide #10.
PN WO200240996-A2.
PD 23-MAY-2002.
PA (MITO-) MITOKOR.
Query Match 3.9%; Score 30; DB 6; Length 323;
Best Local Similarity 52.4%; Pred. No. 1.8e+02;
RESULT 1359
ID ABX05956 standard; DNA; 327 BP.
DE S. pneumoniae type 4 strain coding region #244.
PN WO200277021-A2.
PD 03-OCT-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 3.9%; Score 30; DB 10; Length 327;
Best Local Similarity 59.3%; Pred. No. 1.8e+02;
RESULT 1360
ID AAC19546 standard; cDNA; 372 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 23621.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Query Match 3.9%; Score 30; DB 3; Length 372;
Best Local Similarity 50.7%; Pred. No. 1.9e+02;
RESULT 1361
ID ABX41119 standard; cDNA; 375 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #6284.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 3.9%; Score 30; DB 8; Length 375;
Best Local Similarity 61.5%; Pred. No. 1.9e+02;
RESULT 1362
ID AAA28547 standard; DNA; 382 BP.
DE Human PC-1 gene intron 6/intron 7 partial sequences.
PN WO200029424-A1.
PD 25-MAY-2000.
PA (REGC) UNIV CALIFORNIA.
PA (OSPE-) OSPEDALE CASA SOLLIEVO SOFFERENZA.
PA (UYCA-) UNIV DI CATANIA.
Query Match 3.9%; Score 30; DB 3; Length 382;
Best Local Similarity 59.3%; Pred. No. 1.9e+02;
RESULT 1363
ID AAL02343 standard; cDNA; 429 BP.
DE Human reproductive system related antigen cDNA SEQ ID NO: 2344.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.9%; Score 30; DB 4; Length 429;
Best Local Similarity 54.5%; Pred. No. 2e+02;
RESULT 1364
ID ABA07648 standard; cDNA; 429 BP.
DE Human ovarian and breast cancer associated polynucleotide SEQ ID NO 205.
PN WO200155325-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.9%; Score 30; DB 4; Length 429;
Best Local Similarity 54.5%; Pred. No. 2e+02;
RESULT 1365
ID AAA67557 standard; DNA; 470 BP.
DE Eucalyptus grandis transketolase DNA sequence SEQ ID NO:558.
PN WO200022092-A2.
PD 20-APR-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
Query Match 3.9%; Score 30; DB 3; Length 470;
Best Local Similarity 54.5%; Pred. No. 2.1e+02;
RESULT 1366

ID ABL16003 standard; cDNA; 475 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 42491.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.9%; Score 30; DB 4; Length 475;
Best Local Similarity 64.3%; Pred. No. 2.1e+02;
RESULT 1367
ID ABN61741 standard; cDNA; 594 BP.
DE Human cancer related polynucleotide SEQ ID NO 1708.
PN WO200214500-A2.
PD 21-FEB-2002.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 3.9%; Score 30; DB 6; Length 594;
Best Local Similarity 61.5%; Pred. No. 2.4e+02;
RESULT 1368
ID ACA27794 standard; DNA; 651 BP.
DE Prokaryotic essential gene #9451.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 3.9%; Score 30; DB 8; Length 651;
Best Local Similarity 48.3%; Pred. No. 2.5e+02;
RESULT 1369
ID AAH51629 standard; cDNA; 838 BP.
DE Human g35018 cDNA sequence SEQ ID 38.
PN WO200058510-A2.
PD 05-OCT-2000.
PA (GEST) GENSET.
Query Match 3.9%; Score 30; DB 3; Length 838;
Best Local Similarity 52.4%; Pred. No. 2.8e+02;
RESULT 1370
ID ABN74609 standard; cDNA; 931 BP.
DE Bovine embryonic germ (EG) cell cDNA EST #660.
PN WO200194550-A2.
PD 13-DEC-2001.
PA (INFI-) INFIGEN INC.
Query Match 3.9%; Score 30; DB 6; Length 931;
Best Local Similarity 46.8%; Pred. No. 2.9e+02;
RESULT 1371
ID AAH51630 standard; cDNA; 985 BP.
DE Human g35018 cDNA sequence SEQ ID 39.
PN WO200058510-A2.
PD 05-OCT-2000.
PA (GEST) GENSET.
Query Match 3.9%; Score 30; DB 3; Length 985;
Best Local Similarity 52.4%; Pred. No. 3e+02;
RESULT 1372
ID ABZ83299 standard; cDNA; 1024 BP.
DE Toxicologically relevant human nucleotide sequence #458.
PN WO2003016500-A2.
PD 27-FEB-2003.
PA (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
Query Match 3.9%; Score 30; DB 10; Length 1024;
Best Local Similarity 52.4%; Pred. No. 3e+02;
RESULT 1373
ID ABL28745 standard; DNA; 1047 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 37708.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.9%; Score 30; DB 4; Length 1047;
Best Local Similarity 64.3%; Pred. No. 3.1e+02;
RESULT 1374
ID ABL64399 standard; DNA; 1052 BP.
DE Stomach cancer related gene sequence SEQ ID NO:2736.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 3.9%; Score 30; DB 6; Length 1052;
Best Local Similarity 52.4%; Pred. No. 3.1e+02;
RESULT 1375

ID ABX95118 standard; DNA; 1070 BP.
DE DNA sequence encoding human Biliverdin reductase (BVR) 1 protein.
PN US2003027124-A1.
PD 06-FEB-2003.
PA (MAIN/) MAINES M D.
Query Match 3.9%; Score 30; DB 8; Length 1070;
Best Local Similarity 52.4%; Pred. No. 3.1e+02;
RESULT 1376
ID ACF05667 standard; DNA; 1070 BP.
DE Human biliverdin reductase DNA.
PN WO2003055981-A2.
PD 10-JUL-2003.
PA (UYRP) UNIV ROCHESTER.
Query Match 3.9%; Score 30; DB 9; Length 1070;
Best Local Similarity 52.4%; Pred. No. 3.1e+02;
RESULT 1377
ID AAH51628 standard; cDNA; 1154 BP.
DE Human g35018 cDNA sequence SEQ ID 37.
PN WO200058510-A2.
PD 05-OCT-2000.
PA (GEST) GENSET.
Query Match 3.9%; Score 30; DB 3; Length 1154;
Best Local Similarity 52.4%; Pred. No. 3.2e+02;
RESULT 1378
ID ADH82989 standard; DNA; 1236 BP.
DE Enterococcus faecalis polynucleotide #874.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match 3.9%; Score 30; DB 10; Length 1236;
Best Local Similarity 46.6%; Pred. No. 3.3e+02;
RESULT 1379
ID AAH51627 standard; cDNA; 1301 BP.
DE Human g35018 cDNA sequence SEQ ID 36.
PN WO200058510-A2.
PD 05-OCT-2000.
PA (GEST) GENSET.
Query Match 3.9%; Score 30; DB 3; Length 1301;
Best Local Similarity 52.4%; Pred. No. 3.4e+02;
RESULT 1380
ID AAZ97063 standard; cDNA; 1357 BP.
DE Human secreted protein gene 45 cDNA clone HAGDI35, SEQ ID NO:55.
PN WO9966041-A1.
PD 23-DEC-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.9%; Score 30; DB 3; Length 1357;
Best Local Similarity 45.9%; Pred. No. 3.5e+02;
RESULT 1381
ID ADA39642 standard; cDNA; 1357 BP.
DE Human secreted protein encoding cDNA.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.9%; Score 30; DB 8; Length 1357;
Best Local Similarity 45.9%; Pred. No. 3.5e+02;
RESULT 1382
ID ACH66692 standard; cDNA; 1357 BP.
DE Novel human secreted protein #45 cDNA.
PN US2003065151-A1.
PD 03-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.9%; Score 30; DB 9; Length 1357;
Best Local Similarity 45.9%; Pred. No. 3.5e+02;
RESULT 1383
ID ADC73388 standard; DNA; 1357 BP.
DE Human secreted protein-related DNA - SEQ ID 21.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.9%; Score 30; DB 10; Length 1357;
Best Local Similarity 45.9%; Pred. No. 3.5e+02;
RESULT 1384

ID AAH51631 standard; cDNA; 1386 BP.
DE Human g35018 cDNA sequence SEQ ID 40.
PN WO200058510-A2.
PD 05-OCT-2000.
PA (GEST) GENSET.
Query Match 3.9%; Score 30; DB 3; Length 1386;
Best Local Similarity 52.4%; Pred. No. 3.5e+02;
RESULT 1385
ID AAH72858 standard; cDNA; 1445 BP.
DE Human cervical cancer marker nucleic acid 4132.
PN WO200142467-A2.
PD 14-JUN-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.9%; Score 30; DB 4; Length 1445;
Best Local Similarity 57.4%; Pred. No. 3.6e+02;
RESULT 1386
ID ADL62765 standard; DNA; 1445 BP.
DE Human ovarian cancer DNA marker #20977.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.9%; Score 30; DB 5; Length 1445;
Best Local Similarity 57.4%; Pred. No. 3.6e+02;
RESULT 1387
ID AAF32772 standard; cDNA; 1578 BP.
DE Human secreted protein cDNA #16.
PN WO200077197-A1.
PD 21-DEC-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
Query Match 3.9%; Score 30; DB 4; Length 1578;
Best Local Similarity 50.0%; Pred. No. 3.7e+02;
RESULT 1388
ID ABL09057 standard; cDNA; 1645 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 21653.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.9%; Score 30; DB 4; Length 1645;
Best Local Similarity 48.3%; Pred. No. 3.8e+02;
RESULT 1389
ID ADQ22866 standard; DNA; 1675 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5686.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 3.9%; Score 30; DB 12; Length 1675;
Best Local Similarity 50.7%; Pred. No. 3.8e+02;
RESULT 1390
ID AAL06896 standard; DNA; 1880 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 9584.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.9%; Score 30; DB 4; Length 1880;
Best Local Similarity 54.5%; Pred. No. 4e+02;
RESULT 1391
ID AAL06897 standard; DNA; 1880 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 9585.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.9%; Score 30; DB 4; Length 1880;
Best Local Similarity 54.5%; Pred. No. 4e+02;
RESULT 1392
ID ABA08116 standard; DNA; 1880 BP.
DE Human ovarian and breast cancer associated polynucleotide SEQ ID NO 911.
PN WO200155325-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.9%; Score 30; DB 4; Length 1880;
Best Local Similarity 54.5%; Pred. No. 4e+02;
RESULT 1393

ID ABA08115 standard; DNA; 1880 BP.
DE Human ovarian and breast cancer associated polynucleotide SEQ ID NO 910.
PN WO200155325-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.9%; Score 30; DB 4; Length 1880;
Best Local Similarity 54.5%; Pred. No. 4e+02;
RESULT 1394
ID ADA73281 standard; DNA; 2000 BP.
DE Rice gene, SEQ ID 6607.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 3.9%; Score 30; DB 8; Length 2000;
Best Local Similarity 67.7%; Pred. No. 4.2e+02;
RESULT 1395
ID ADJ41527 standard; cDNA; 2000 BP.
DE Plant cDNA #2527.
PN US2004016025-A1.
PD 22-JAN-2004.
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICKE D.
PA (ZHUT/) ZHU T.
Query Match 3.9%; Score 30; DB 12; Length 2000;
Best Local Similarity 52.4%; Pred. No. 4.2e+02;
RESULT 1396
ID ADA31173 standard; DNA; 2007 BP.
DE DNA encoding Acinetobacter baumannii protein #2460.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 3.9%; Score 30; DB 9; Length 2007;
Best Local Similarity 51.5%; Pred. No. 4.2e+02;
RESULT 1397
ID ADQ24884 standard; DNA; 2291 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7704.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 3.9%; Score 30; DB 12; Length 2291;
Best Local Similarity 50.7%; Pred. No. 4.4e+02;
RESULT 1398
ID AAK81968 standard; DNA; 2514 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36780.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.9%; Score 30; DB 4; Length 2514;
Best Local Similarity 57.4%; Pred. No. 4.6e+02;
RESULT 1399
ID ADO61722 standard; DNA; 2721 BP.
DE Transcription factor G1206 coding sequence, SEQ ID 189.
PN WO2004031349-A2.
PD 15-APR-2004.
PA (MEND-) MENDEL BIOTECHNOLOGY INC.
Query Match 3.9%; Score 30; DB 12; Length 2721;
Best Local Similarity 54.5%; Pred. No. 4.8e+02;
RESULT 1400
ID ABL17257 standard; DNA; 2830 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 3244.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.9%; Score 30; DB 4; Length 2830;
Best Local Similarity 48.3%; Pred. No. 4.9e+02;

RESULT 1401
ID ABL17175 standard; DNA; 2980 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 2998.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.9%; Score 30; DB 4; Length 2980;
Best Local Similarity 48.3%; Pred. No. 5e+02;
RESULT 1402
ID ABL16002 standard; cDNA; 3195 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 42488.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.9%; Score 30; DB 4; Length 3195;
Best Local Similarity 64.3%; Pred. No. 5.2e+02;
RESULT 1403
ID AAF16145 standard; cDNA; 4006 BP.
DE Human prostate cancer antigen nucleotide sequence SEQ ID NO:580.
PN WO200055174-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
Query Match 3.9%; Score 30; DB 3; Length 4006;
Best Local Similarity 45.9%; Pred. No. 5.8e+02;
RESULT 1404
ID ABA07203 standard; DNA; 4338 BP.
DE Human pancreatic cancer related genomic DNA, SEQ ID NO: 522.
PN WO200155206-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.9%; Score 30; DB 4; Length 4338;
Best Local Similarity 61.5%; Pred. No. 6e+02;
RESULT 1405
ID AAK89835 standard; DNA; 4338 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 3411.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.9%; Score 30; DB 4; Length 4338;
Best Local Similarity 61.5%; Pred. No. 6e+02;
RESULT 1406
ID ABA06871 standard; DNA; 4338 BP.
DE Human polynucleotide SEQ ID NO 27.
PN WO200155205-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.9%; Score 30; DB 4; Length 4338;
Best Local Similarity 61.5%; Pred. No. 6e+02;
RESULT 1407
ID ACA61956 standard; DNA; 4338 BP.
DE DNA encoding human HVADT77 protein #1.
PN US2003044890-A1.
PD 06-MAR-2003.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 3.9%; Score 30; DB 10; Length 4338;
Best Local Similarity 61.5%; Pred. No. 6e+02;
RESULT 1408
ID ABL09056 standard; cDNA; 4408 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 21650.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.9%; Score 30; DB 4; Length 4408;
Best Local Similarity 48.3%; Pred. No. 6e+02;
RESULT 1409
ID AAK75249 standard; DNA; 4447 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:30061.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match
Best Local Similarity 3.9%; Score 30; DB 4; Length 4447;
RESULT 1410
ID ABL17256 standard; DNA; 5367 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 3241.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match
Best Local Similarity 3.9%; Score 30; DB 4; Length 5367;
RESULT 1411
ID ABL17174 standard; DNA; 5397 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 2995.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match
Best Local Similarity 3.9%; Score 30; DB 4; Length 5397;
RESULT 1412
ID ABL29956 standard; DNA; 6429 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 41341.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match
Best Local Similarity 3.9%; Score 30; DB 4; Length 6429;
RESULT 1413
ID ABL15594 standard; cDNA; 6436 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 41264.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match
Best Local Similarity 3.9%; Score 30; DB 4; Length 6436;
RESULT 1414
ID AAV52144 standard; DNA; 8148 BP.
DE Streptococcus pneumoniae genome fragment SEQ ID NO:11.
PN WO9818931-A2.
PD 07-MAY-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 3.9%; Score 30; DB 2; Length 8148;
RESULT 1415
ID ABL32113 standard; DNA; 9927 BP.
DE Human immune system associated gene SEQ ID NO: 86.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 3.9%; Score 30; DB 6; Length 9927;
RESULT 1416
ID AAX13081 standard; DNA; 12860 BP.
DE Enterococcus faecalis genome contig SEQ ID NO:144.
PN WO9850555-A2.
PD 12-NOV-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 3.9%; Score 30; DB 2; Length 12860;
RESULT 1417
ID ABS98876 standard; DNA; 12860 BP.
DE Enterococcus faecalis contig sequence #144.
PN US2002120116-A1.
PD 29-AUG-2002.
PA (KUNS/) KUNSCH C A.
PA (DILL/) DILLON P J.
PA (BARA/) BARASH S.
Query Match
Best Local Similarity 3.9%; Score 30; DB 6; Length 12860;
RESULT 1418
ID ABL28744 standard; DNA; 14197 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 37705.
PN WO200171042-A2.
PD 27-SEP-2001.

PA (PEKE) PE CORP NY.
Query Match
Best Local Similarity 3.9%; Score 30; DB 4; Length 14197;
RESULT 1419
ID AAK73103 standard; DNA; 15196 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27915.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 3.9%; Score 30; DB 4; Length 15196;
RESULT 1420
ID AAK87548 standard; DNA; 15196 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:42360.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 3.9%; Score 30; DB 4; Length 15196;
RESULT 1421
ID ABL32313 standard; DNA; 18683 BP.
DE Human immune system associated gene SEQ ID NO: 286.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 3.9%; Score 30; DB 6; Length 18683;
RESULT 1422
ID ABL54334 standard; DNA; 18683 BP.
DE Chemically treated apoptosis gene complementary to gene #17.
PN WO200177164-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 3.9%; Score 30; DB 6; Length 18683;
RESULT 1423
ID ADO79402 standard; DNA; 76600 BP.
DE DLG1 region, SEQ ID 1.
PN WO2004047514-A2.
PD 10-JUN-2004.
PA (SEQU-) SEQUENOM INC.
Query Match
Best Local Similarity 3.9%; Score 30; DB 12; Length 76600;
RESULT 1424
Query Match
Best Local Similarity 3.9%; Score 30; DB 12; Length 89378;
RESULT 1425
Query Match
Best Local Similarity 3.9%; Score 30; DB 12; Length 89378;
RESULT 1426
Query Match
Best Local Similarity 3.9%; Score 30; DB 12; Length 89378;
RESULT 1427
Query Match
Best Local Similarity 3.9%; Score 30; DB 6; Length 110000;
RESULT 1428
Query Match
Best Local Similarity 3.9%; Score 30; DB 10; Length 110000;
RESULT 1429
ID ADN47591 standard; DNA; 2089378 BP.
DE Thermococcus kodakaraensis KOD1 genome DNA sequence SeqID1469.
PN WO2004022736-A1.
PD 18-MAR-2004.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match
Best Local Similarity 3.9%; Score 30; DB 12; Length 110000;
RESULT 1430
ID ADN47209 standard; DNA; 2089378 BP.
DE Thermococcus kodakaraensis KOD1 genome DNA sequence SeqID1087.
PN WO2004022736-A1.
PD 18-MAR-2004.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match
Best Local Similarity 3.9%; Score 30; DB 12; Length 110000;

Best Local Similarity 61.5%; Pred. No. 2.6e+03;
RESULT 1431
ID ADN47960 standard; DNA; 2089378 BP.
DE Thermococcus kodakaraensis KOD1 genome DNA sequence SeqID1838.
PN WO2004022736-A1.
PD 18-MAR-2004.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match 3.9%; Score 30; DB 12; Length 110000;
Best Local Similarity 61.5%; Pred. No. 2.6e+03;
RESULT 1432
ID ABK83461 standard; cDNA; 128600 BP.
DE Human cDNA differentially expressed in granulocytic cells #32.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 3.9%; Score 30; DB 6; Length 128600;
Best Local Similarity 50.7%; Pred. No. 2.8e+03;
RESULT 1433
ID ABK83574 standard; cDNA; 147419 BP.
DE Human cDNA differentially expressed in granulocytic cells #145.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 3.9%; Score 30; DB 6; Length 147419;
Best Local Similarity 51.5%; Pred. No. 3e+03;
RESULT 1434
ID ADG86300 standard; DNA; 220756 BP.
DE Human SMRT partial genomic DNA sequence SEQ ID NO:14.
PN WO2003106645-A2.
PD 24-DEC-2003.
PA (ISIS-) ISIS PHARM INC.
Query Match 3.9%; Score 30; DB 12; Length 220756;
Best Local Similarity 50.7%; Pred. No. 3.5e+03;
RESULT 1435
ID ADD25213 standard; DNA; 271990 BP.
DE Fertility restorer protein genomic DNA sequence.
PN WO2003006622-A2.
PD 23-JAN-2003.
PA (UYMC-) UNIV MCGILL.
PA (DNAL-) DNA LANDMARKS INC.
Query Match 3.9%; Score 30; DB 10; Length 271990;
Best Local Similarity 59.3%; Pred. No. 3.7e+03;
RESULT 1436
ID ADN61228 standard; DNA; 271990 BP.
DE Radish nuclear fertility restorer Rfo locus SEQ ID NO:87.
PN WO2004006655-A2.
PD 22-JAN-2004.
PA (UYMC-) UNIV MCGILL.
PA (DNAL-) DNA LANDMARKS INC.
PA (BADI) BASF PLANT SCI GMBH.
Query Match 3.9%; Score 30; DB 12; Length 271990;
Best Local Similarity 59.3%; Pred. No. 3.7e+03;
RESULT 1437
ID AAH51601 standard; DNA; 319608 BP.
DE Human chromosome 13q31-q33 genomic nucleotide sequence.
PN WO200058510-A2.
PD 05-OCT-2000.
PA (GEST) GENSET.
Query Match 3.9%; Score 30; DB 3; Length 319608;
Best Local Similarity 52.4%; Pred. No. 3.9e+03;
RESULT 1438
ID AAS09301 standard; DNA; 319608 BP.
DE Human schizophrenia associated gene g35030 and biallelic markers A1-A71.
Query Match 3.9%; Score 30; DB 5; Length 319608;
Best Local Similarity 52.4%; Pred. No. 3.9e+03;
RESULT 1439
ID ABX89084 standard; cDNA; 298 BP.
DE Corn ear-derived polynucleotide (cpd) #7544.
PN US6476212-B1.
PD 05-NOV-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 3.9%; Score 29.8; DB 10; Length 298;
Best Local Similarity 60.5%; Pred. No. 2e+02;

RESULT 1440
ID ABV11776 standard; cDNA; 377 BP.
DE Human prostate expression marker cDNA 11767.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.9%; Score 29.8; DB 5; Length 377;
Best Local Similarity 52.9%; Pred. No. 2.2e+02;
RESULT 1441
ID AAK67152 standard; DNA; 405 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21964.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.9%; Score 29.8; DB 4; Length 405;
Best Local Similarity 45.8%; Pred. No. 2.3e+02;
RESULT 1442
ID ABV32921 standard; cDNA; 417 BP.
DE Human prostate expression marker cDNA 32912.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.9%; Score 29.8; DB 5; Length 417;
Best Local Similarity 52.9%; Pred. No. 2.3e+02;
RESULT 1443
ID ABV86769 standard; cDNA; 434 BP.
DE Human colon cancer related cDNA SEQ ID NO 80.
PN WO200258534-A2.
PD 01-AUG-2002.
PA (CORI-) CORIXA CORP.
Query Match 3.9%; Score 29.8; DB 6; Length 434;
Best Local Similarity 55.2%; Pred. No. 2.3e+02;
RESULT 1444
ID ABV86980 standard; cDNA; 519 BP.
DE Human colon cancer related cDNA SEQ ID NO 291.
PN WO200258534-A2.
PD 01-AUG-2002.
PA (CORI-) CORIXA CORP.
Query Match 3.9%; Score 29.8; DB 6; Length 519;
Best Local Similarity 55.2%; Pred. No. 2.5e+02;
RESULT 1445
ID AAA16422 standard; DNA; 567 BP.
DE Human colon cancer differentially expressed nucleotide sequence #427.
PN WO200012702-A2.
PD 09-MAR-2000.
PA (FARB) BAYER CORP.
Query Match 3.9%; Score 29.8; DB 3; Length 567;
Best Local Similarity 59.7%; Pred. No. 2.7e+02;
RESULT 1446
ID ABV87337 standard; cDNA; 580 BP.
DE Human colon cancer related cDNA SEQ ID NO 648.
PN WO200258534-A2.
PD 01-AUG-2002.
PA (CORI-) CORIXA CORP.
Query Match 3.9%; Score 29.8; DB 6; Length 580;
Best Local Similarity 55.2%; Pred. No. 2.7e+02;
RESULT 1447
ID AAC53674 standard; DNA; 678 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 75318.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 3.9%; Score 29.8; DB 3; Length 678;
Best Local Similarity 47.2%; Pred. No. 2.9e+02;
RESULT 1448
ID ADI30720 standard; cDNA; 704 BP.
DE Human cDNA #46.
PN US6607879-B1.
PD 19-AUG-2003.
PA (INCY-) INCYTE CORP.
Query Match 3.9%; Score 29.8; DB 11; Length 704;
Best Local Similarity 50.4%; Pred. No. 2.9e+02;
RESULT 1449
ID AAI95633 standard; cDNA; 757 BP.

```
DE Human neuroblastoma expressed polynucleotide SEQ ID NO 1708.
PN WO200166719-A1.
PD 13-SEP-2001.
PA (CHIB-) CHIBA PREFECTURE.
PA (HISM) HISAMITSU PHARM CO LTD.
  Query Match 3.9%; Score 29.8; DB 4; Length 757;
  Best Local Similarity 58.4%; Pred. No. 3e+02;
RESULT 1450
ID AA215504 standard; cDNA; 760 BP.
DE Human gene expression product cDNA sequence SEQ ID NO:2973.
PN WO938972-A2.
PD 05-AUG-1999.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
  Query Match 3.9%; Score 29.8; DB 2; Length 760;
  Best Local Similarity 55.0%; Pred. No. 3e+02;
RESULT 1451
ID ABV05980 standard; cDNA; 833 BP.
DE Human prostate expression marker cDNA 5971.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match 3.9%; Score 29.8; DB 5; Length 833;
  Best Local Similarity 44.1%; Pred. No. 3.2e+02;
RESULT 1452
ID AAC34752 standard; DNA; 902 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 7764.
PN EP1033405-A2.
PD 06-SEP-2000.
  Query Match 3.9%; Score 29.8; DB 3; Length 902;
  Best Local Similarity 51.1%; Pred. No. 3.3e+02;
RESULT 1453
ID ABQ33943 standard; DNA; 1126 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 20534.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
  Query Match 3.9%; Score 29.8; DB 6; Length 1126;
  Best Local Similarity 49.7%; Pred. No. 3.7e+02;
RESULT 1454
ID ABQ33942 standard; DNA; 1126 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 20533.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
  Query Match 3.9%; Score 29.8; DB 6; Length 1126;
  Best Local Similarity 49.7%; Pred. No. 3.7e+02;
RESULT 1455
ID ADD49054 standard; DNA; 1157 BP.
DE Human NOV7a coding sequence, SEQ ID 27.
PN WO2003060149-A2.
PD 24-JUL-2003.
PA (CURA-) CURAGEN CORP.
  Query Match 3.9%; Score 29.8; DB 10; Length 1157;
  Best Local Similarity 55.2%; Pred. No. 3.7e+02;
RESULT 1456
ID AAC37127 standard; DNA; 1213 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 16274.
PN EP1033405-A2.
PD 06-SEP-2000.
  Query Match 3.9%; Score 29.8; DB 3; Length 1213;
  Best Local Similarity 51.1%; Pred. No. 3.8e+02;
RESULT 1457
ID ADJ75145 standard; DNA; 1310 BP.
DE Marker gene SEQ ID NO:397.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
  Query Match 3.9%; Score 29.8; DB 12; Length 1310;
  Best Local Similarity 55.2%; Pred. No. 3.9e+02;
RESULT 1458
ID ADN04566 standard; cDNA; 1310 BP.
DE Antipsoriatic cDNA sequence #487.
PN WO200171042-A2.
  Query Match 3.9%; Score 29.8; DB 10; Length 1550;
  Best Local Similarity 55.2%; Pred. No. 4.2e+02;
RESULT 1467
ID ABL27423 standard; DNA; 1596 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 33742.
PN WO200171042-A2.
  Query Match 3.9%; Score 29.8; DB 12; Length 1310;
  Best Local Similarity 55.2%; Pred. No. 3.9e+02;
RESULT 1459
ID AAQ75377 standard; DNA; 1316 BP.
DE Human elastase inhibitor gene.
PN US5370991-A.
PD 06-DEC-1994.
PA (BLOO-) CENT BLOOD RES INC.
  Query Match 3.9%; Score 29.8; DB 2; Length 1316;
  Best Local Similarity 55.2%; Pred. No. 3.9e+02;
RESULT 1460
ID AAT14255 standard; cDNA; 1316 BP.
DE Human elastase inhibitor cDNA.
PN WO9610418-A1.
PD 11-APR-1996.
PA (BLOO-) CENT BLOOD RES INC.
  Query Match 3.9%; Score 29.8; DB 2; Length 1316;
  Best Local Similarity 55.2%; Pred. No. 3.9e+02;
RESULT 1461
ID ABL69984 standard; DNA; 1316 BP.
DE Pancreas cancer related gene sequence SEQ ID NO:8321.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
  Query Match 3.9%; Score 29.8; DB 6; Length 1316;
  Best Local Similarity 55.2%; Pred. No. 3.9e+02;
RESULT 1462
ID ABK84121 standard; cDNA; 1316 BP.
DE Human cDNA differentially expressed in granulocytic cells #692.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
  Query Match 3.9%; Score 29.8; DB 6; Length 1316;
  Best Local Similarity 55.2%; Pred. No. 3.9e+02;
RESULT 1463
ID ACA56112 standard; cDNA; 1430 BP.
DE Horse signalling pathway polynucleotide probe SEQ ID NO 710.
PN US6500938-B1.
PD 31-DEC-2002.
PA (INCY-) INCYTE GENOMICS INC.
  Query Match 3.9%; Score 29.8; DB 10; Length 1430;
  Best Local Similarity 55.2%; Pred. No. 4.1e+02;
RESULT 1464
ID ADI55908 standard; DNA; 1430 BP.
DE Human polynucleotide probe #710.
PN US2004010136-A1.
PD 15-JAN-2004.
PA (INCY-) INCYTE GENOMICS INC.
  Query Match 3.9%; Score 29.8; DB 12; Length 1430;
  Best Local Similarity 55.2%; Pred. No. 4.1e+02;
RESULT 1465
ID ABZ35236 standard; cDNA; 1458 BP.
DE Human gene expression profile polynucleotide SEQ ID NO 347.
PN WO200274979-A2.
PD 26-SEP-2002.
PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.
  Query Match 3.9%; Score 29.8; DB 6; Length 1458;
  Best Local Similarity 55.2%; Pred. No. 4.1e+02;
RESULT 1466
ID ADD49056 standard; DNA; 1550 BP.
DE Human NOV7b coding sequence, SEQ ID 29.
PN WO2003060149-A2.
PD 24-JUL-2003.
PA (CURA-) CURAGEN CORP.
  Query Match 3.9%; Score 29.8; DB 10; Length 1550;
  Best Local Similarity 55.2%; Pred. No. 4.2e+02;
RESULT 1467
ID ABL27423 standard; DNA; 1596 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 33742.
PN WO200171042-A2.
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PD 27-SEP-2001.
PA (PEKE) PE CORP NY. 3.9%; Score 29.8; DB 4; Length 1596;
Query Match 58.4%; Pred. No. 4.3e+02;
Best Local Similarity 58.4%; Pred. No. 4.3e+02;
RESULT 1468
ID ADF81744 standard; DNA; 1829 BP.
DE Leukaemia-related DNA sequence #2300.
PN WO2003039443-A2.
PD 15-MAY-2003.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA (UYLU-) UNIV LUDWIG MAXIMILIANS.
PA (HAPE/) HAERLACH T.
PA (SCHO/) SCHOCH C.
PA (KERN/) KERN W.
Query Match 3.9%; Score 29.8; DB 10; Length 1829;
Best Local Similarity 55.2%; Pred. No. 4.6e+02;
RESULT 1469
ID AAC77964 standard; cDNA; 1931 BP.
DE Human cancer associated gene sequence SEQ ID NO:358.
PN WO2000055350-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.9%; Score 29.8; DB 3; Length 1931;
Best Local Similarity 55.2%; Pred. No. 4.7e+02;
RESULT 1470
ID ADN04631 standard; cDNA; 2634 BP.
DE Antipsoriatic cDNA sequence #525.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 3.9%; Score 29.8; DB 12; Length 2634;
Best Local Similarity 55.2%; Pred. No. 5.4e+02;
RESULT 1471
ID ADJ58237 standard; DNA; 2883 BP.
DE Urease subunit polypeptide complex encoding sequence.
PN EP1176192-A2.
PD 30-JAN-2002.
PA (ALKU) AKZO NOBEL NV.
Query Match 3.9%; Score 29.8; DB 7; Length 2883;
Best Local Similarity 51.9%; Pred. No. 5.7e+02;
RESULT 1472
ID ABS53210 standard; cDNA; 3497 BP.
DE Human mitogen-activated protein kinase (MKK) 4alpha cDNA.
PN US2002102691-A1.
PD 01-AUG-2002.
PA (UYMA-) UNIV MASSACHUSETTS.
Query Match 3.9%; Score 29.8; DB 6; Length 3497;
Best Local Similarity 46.4%; Pred. No. 6.2e+02;
RESULT 1473
ID ABL27422 standard; DNA; 3596 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 33739.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.9%; Score 29.8; DB 4; Length 3596;
Best Local Similarity 58.4%; Pred. No. 6.3e+02;
RESULT 1474
ID ABL02829 standard; cDNA; 3831 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 2969.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.9%; Score 29.8; DB 4; Length 3831;
Best Local Similarity 52.9%; Pred. No. 6.5e+02;
RESULT 1475
ID ABA09585 standard; DNA; 4464 BP.
DE Human bone marrow expressed oligonucleotide SEQ ID NO: 11.
PN WO200174836-A1.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 3.9%; Score 29.8; DB 5; Length 4464;
Best Local Similarity 51.1%; Pred. No. 7e+02;
RESULT 1476

ID ABA09669 standard; DNA; 4485 BP.
DE Human bone marrow expressed oligonucleotide SEQ ID NO: 178.
PN WO200174836-A1.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 3.9%; Score 29.8; DB 5; Length 4485;
Best Local Similarity 51.1%; Pred. No. 7e+02;
RESULT 1477
ID ABL20936 standard; DNA; 4747 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 14281.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.9%; Score 29.8; DB 4; Length 4747;
Best Local Similarity 56.7%; Pred. No. 7.2e+02;
RESULT 1478
ID AAK78479 standard; DNA; 4807 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33291.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.9%; Score 29.8; DB 4; Length 4807;
Best Local Similarity 49.8%; Pred. No. 7.2e+02;
RESULT 1479
ID ABN80116 standard; DNA; 6036 BP.
DE Human chemically modified disease associated gene SEQ ID NO 133.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.9%; Score 29.8; DB 6; Length 6036;
Best Local Similarity 55.2%; Pred. No. 8e+02;
RESULT 1480
ID ABL02828 standard; cDNA; 6103 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 2966.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.9%; Score 29.8; DB 4; Length 6103;
Best Local Similarity 52.9%; Pred. No. 8.1e+02;
RESULT 1481
ID ABL34014 standard; DNA; 6182 BP.
DE Human immune system associated gene SEQ ID NO: 1987.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.9%; Score 29.8; DB 6; Length 6182;
Best Local Similarity 51.1%; Pred. No. 8.1e+02;
RESULT 1482
ID ABL19982 standard; DNA; 6362 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 11419.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.9%; Score 29.8; DB 4; Length 6362;
Best Local Similarity 56.7%; Pred. No. 8.2e+02;
RESULT 1483
ID ABL32966 standard; DNA; 6381 BP.
DE Human immune system associated gene SEQ ID NO: 939.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.9%; Score 29.8; DB 6; Length 6381;
Best Local Similarity 49.7%; Pred. No. 8.2e+02;
RESULT 1484
ID ABL34518 standard; DNA; 6381 BP.
DE Human metastasis associated gene SEQ ID NO: 71.
PN WO200177376-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.9%; Score 29.8; DB 6; Length 6381;
Best Local Similarity 49.7%; Pred. No. 8.2e+02;
RESULT 1485
ID ABL70243 standard; DNA; 6381 BP.

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DE Chemically treated cell signalling DNA sequence#67.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
  Query Match 3.9%; Score 29.8; DB 6; Length 6381;
  Best Local Similarity 49.7%; Pred. No. 8.2e+02;
  RESULT 1486
ID AAS18540 standard; DNA; 8145 BP.
DE Partial galanin receptor (GALR1) gene sequence #2.
PN WO200179237-A2.
PD 25-OCT-2001.
PA (GENA-) GENAISSANCE PHARM INC.
  Query Match 3.9%; Score 29.8; DB 6; Length 8145;
  Best Local Similarity 51.9%; Pred. No. 9.2e+02;
  RESULT 1487
ID ABL01872 standard; cDNA; 8542 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 98.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
  Query Match 3.9%; Score 29.8; DB 4; Length 8542;
  Best Local Similarity 56.7%; Pred. No. 9.4e+02;
  RESULT 1488
ID AAS45503 standard; DNA; 8996 BP.
DE Chemically pretreated complementary DNA associated with cell cycle #104.
PN WO200168911-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
  Query Match 3.9%; Score 29.8; DB 4; Length 8996;
  Best Local Similarity 51.1%; Pred. No. 9.7e+02;
  RESULT 1489
ID ABK28435 standard; DNA; 8996 BP.
DE DNA transcription associated genomic DNA #155.
PN WO200192565-A2.
PD 06-DEC-2001.
PA (EPIG-) EPIGENOMICS AG.
  Query Match 3.9%; Score 29.8; DB 6; Length 8996;
  Best Local Similarity 51.1%; Pred. No. 9.7e+02;
  RESULT 1490
ID ABL32343 standard; DNA; 11534 BP.
DE Human immune system associated gene SEQ ID NO: 316.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
  Query Match 3.9%; Score 29.8; DB 6; Length 11534;
  Best Local Similarity 43.3%; Pred. No. 1.1e+03;
  RESULT 1491
ID ADB54329 standard; DNA; 11787 BP.
DE Pretreated genomic DNA region 253.
PN WO2003072821-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
  Query Match 3.9%; Score 29.8; DB 10; Length 11787;
  Best Local Similarity 49.7%; Pred. No. 1.1e+03;
  RESULT 1492
ID ABL15354 standard; cDNA; 13075 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 40544.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
  Query Match 3.9%; Score 29.8; DB 4; Length 13075;
  Best Local Similarity 51.9%; Pred. No. 1.2e+03;
  RESULT 1493
ID ABL33227 standard; DNA; 13125 BP.
DE Human immune system associated gene SEQ ID NO: 1200.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
  Query Match 3.9%; Score 29.8; DB 6; Length 13125;
  Best Local Similarity 45.2%; Pred. No. 1.2e+03;
  RESULT 1494
ID ABL34557 standard; DNA; 13125 BP.
DE Human metastasis associated gene SEQ ID NO: 110.
PN WO200177376-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
  Query Match 3.9%; Score 29.8; DB 6; Length 13125;
  Best Local Similarity 45.2%; Pred. No. 1.2e+03;
  RESULT 1495
ID ABL70284 standard; DNA; 13125 BP.
DE Chemically treated cell signalling DNA sequence complementary to#87.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
  Query Match 3.9%; Score 29.8; DB 6; Length 13125;
  Best Local Similarity 45.2%; Pred. No. 1.2e+03;
  RESULT 1496
ID ABZ74645 standard; DNA; 17646 BP.
DE Secreted protein gene 381 genomic fragment HE2CA60, SEQ ID NO:1792.
PN WO200277013-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
  Query Match 3.9%; Score 29.8; DB 8; Length 17646;
  Best Local Similarity 58.4%; Pred. No. 1.3e+03;
  RESULT 1497
ID ADA98997 standard; DNA; 17646 BP.
DE Human secreted protein-related DNA sequence #590.
PN WO2003004623-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
  Query Match 3.9%; Score 29.8; DB 8; Length 17646;
  Best Local Similarity 58.4%; Pred. No. 1.3e+03;
  RESULT 1498
ID ABT17023 standard; DNA; 17646 BP.
DE Human secreted protein-related DNA sequence - SEQ ID No 377.
PN WO200277188-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
  Query Match 3.9%; Score 29.8; DB 10; Length 17646;
  Best Local Similarity 58.4%; Pred. No. 1.3e+03;
  RESULT 1499
ID ABZ68163 standard; DNA; 17646 BP.
DE Human secreted protein encoding genomic DNA SEQ ID NO 1686.
PN WO200277186-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
  Query Match 3.9%; Score 29.8; DB 10; Length 17646;
  Best Local Similarity 58.4%; Pred. No. 1.3e+03;
  RESULT 1500
ID ABL32793 standard; DNA; 19087 BP.
DE Human immune system associated gene SEQ ID NO: 766.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
  Query Match 3.9%; Score 29.8; DB 6; Length 19087;
  Best Local Similarity 49.7%; Pred. No. 1.4e+03;
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OM nucleic - nucleic search, using sw model

Run on: January 24, 2005, 19:07:47 ; Search time 67 Seconds
(without alignments)
8126.333 Million cell updates/sec

Title: US-10-063-553-47
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	43.8	5.7	1141	4	US-09-806-708B-22
C 2	38.2	5.0	7218	1	US-08-232-463-14
C 3	36.4	4.8	369	4	US-09-107-532A-3165
C 4	35.8	4.7	393	4	US-09-583-110-486
C 5	35.8	4.7	832	4	US-09-621-976-2813
C 6	34.8	4.5	1809	4	US-09-589-733C-5
C 7	34.2	4.5	786431	4	US-09-751-389-3
C 8	33.6	4.4	1284	4	US-09-248-796A-2331
C 9	33.2	4.3	1055	4	US-09-806-708B-23
C 10	33	4.3	609	4	US-09-248-796A-6609
C 11	33	4.3	3103	4	US-09-710-279-3462
C 12	33	4.3	3438	4	US-09-710-279-4241
C 13	33	4.3	3463	4	US-09-710-279-3997
C 14	32.4	4.2	746	3	US-08-998-416-270
C 15	32.2	4.2	414	4	US-09-513-999C-1082
C 16	32.2	4.2	855	4	US-09-552-204A-10
C 17	32	4.2	1141	4	US-09-806-708B-22
C 18	32	4.2	4954	1	US-08-920-812-18
C 19	32	4.2	4954	1	US-08-920-827-18
C 20	32	4.2	4954	1	US-08-921-177-18
C 21	32	4.2	4954	1	US-08-362-577C-18
C 22	32	4.2	4954	2	US-08-920-828-18
C 23	32	4.2	11015	4	US-10-204-708-56
C 24	31.8	4.2	894	4	US-09-976-594-90
C 25	31.8	4.2	640681	4	US-09-790-988-1
C 26	31.6	4.1	855	4	US-09-248-796A-4821
C 27	31.4	4.1	425	4	US-09-621-976-8306

C 28	31.4	4.1	572	4	US-09-270-767-8919	Sequence 8919, Ap
C 29	31.4	4.1	572	4	US-09-270-767-24201	Sequence 24201, A
C 30	31.4	4.1	705	4	US-09-248-796A-1388	Sequence 1388, Ap
C 31	31.4	4.1	790	6	5194596-8	Patent No. 5194596
C 32	31.4	4.1	1313	4	US-09-149-476-112	Sequence 112, App
C 33	31.4	4.1	1944	4	US-09-149-476-144	Sequence 144, App
C 34	31.4	4.1	2307	4	US-09-792-024-43	Sequence 43, Appl
C 35	31.4	4.1	4562	4	US-09-620-312D-418	Sequence 418, App
C 36	31.2	4.1	452	4	US-09-621-976-9007	Sequence 9007, Ap
C 37	31.2	4.1	832	4	US-09-621-976-2813	Sequence 2813, Ap
C 38	31.2	4.1	1413	4	US-09-328-352-435	Sequence 435, App
C 39	31.2	4.1	6450	3	US-09-041-886-34	Sequence 34, Appl
C 40	31.2	4.1	6450	4	US-08-453-998-1	Sequence 1, Appli
C 41	31.2	4.1	6450	4	US-10-027-983-3	Sequence 3, Appli
C 42	31.2	4.1	8566	4	US-10-027-983-10	Sequence 10, Appl
C 43	31.2	4.1	392000	4	US-10-027-983-11	Sequence 11, Appl
C 44	31	4.0	389	4	US-09-513-999C-33847	Sequence 33847, A
C 45	31	4.0	399	4	US-09-621-976-8976	Sequence 8976, Ap
C 46	31	4.0	1514	4	US-09-270-767-25648	Sequence 25648, A
C 47	31	4.0	4140	4	US-09-270-767-10280	Sequence 10280, A
C 48	30.8	4.0	427	4	US-09-702-705-1152	Sequence 1152, Ap
C 49	30.8	4.0	427	4	US-09-736-457-1152	Sequence 1152, Ap
C 50	30.8	4.0	427	4	US-09-614-124B-1152	Sequence 1152, Ap
C 51	30.8	4.0	427	4	US-09-671-325-1152	Sequence 1152, Ap
C 52	30.8	4.0	427	4	US-09-658-824-1152	Sequence 1152, Ap
C 53	30.8	4.0	2248	4	US-09-221-013A-1	Sequence 1, Appli
C 54	30.6	4.0	347	4	US-09-513-999C-31729	Sequence 31729, A
C 55	30.6	4.0	1354	4	US-09-799-451-465	Sequence 465, App
C 56	30.6	4.0	2981	1	US-08-257-073-2	Sequence 2, Appli
C 57	30.6	4.0	2981	2	US-08-184-009-119	Sequence 119, App
C 58	30.6	4.0	2981	2	US-08-458-356-119	Sequence 119, App
C 59	30.6	4.0	2981	3	US-08-460-736-119	Sequence 119, App
C 60	30.6	4.0	2981	4	US-09-535-370-119	Sequence 119, App
C 61	30.6	4.0	2981	4	US-09-663-667-119	Sequence 119, App
C 62	30.6	4.0	3107	3	US-08-213-419B-1	Sequence 1, Appli
C 63	30.6	4.0	6124	3	US-08-213-419B-3	Sequence 3, Appli
C 64	30.6	4.0	6578	1	US-08-514-975B-1	Sequence 1, Appli
C 65	30.6	4.0	6578	5	PCT-US95-12507-1	Sequence 1, Appli
C 66	30.6	4.0	15222	2	US-08-801-898A-23	Sequence 23, Appl
C 67	30.6	4.0	15222	3	US-08-962-690-12	Sequence 12, Appl
C 68	30.6	4.0	15223	2	US-08-892-403A-1	Sequence 1, Appli
C 69	30.6	4.0	15223	3	US-08-720-132-1	Sequence 1, Appli
C 70	30.6	4.0	15223	4	US-09-291-894-1	Sequence 1, Appli
C 71	30.6	4.0	15223	4	US-09-847-173-1	Sequence 1, Appli
C 72	30.6	4.0	580073	4	US-08-545-528D-1	Sequence 1, Appli
C 73	30.4	4.0	1265	3	US-08-991-789A-169	Sequence 169, App
C 74	30.4	4.0	1265	3	US-09-062-451-169	Sequence 169, App
C 75	30.4	4.0	1265	4	US-09-598-326-169	Sequence 169, App
C 76	30.4	4.0	1265	4	US-09-289-198-169	Sequence 169, App
C 77	30.4	4.0	1265	4	US-09-429-755-169	Sequence 169, App
C 78	30.4	4.0	7159	4	US-08-956-171E-302	Sequence 302, App
C 79	30.4	4.0	7159	4	US-08-781-986A-302	Sequence 302, App
C 80	30.4	4.0	118067	4	US-09-497-855A-32	Sequence 32, Appl
C 81	30.4	4.0	580073	4	US-08-545-528D-1	Sequence 1, Appli
C 82	30.2	3.9	207	4	US-09-248-796A-10207	Sequence 10207, A
C 83	30.2	3.9	442	4	US-09-513-999C-10609	Sequence 10609, A
C 84	30.2	3.9	572	4	US-09-702-705-606	Sequence 606, App
C 85	30.2	3.9	572	4	US-09-736-457-606	Sequence 606, App
C 86	30.2	3.9	572	4	US-09-614-124B-606	Sequence 606, App
C 87	30.2	3.9	572	4	US-09-671-325-606	Sequence 606, App
C 88	30.2	3.9	572	4	US-09-589-184-606	Sequence 606, App
C 89	30.2	3.9	572	4	US-09-658-824-606	Sequence 606, App
C 90	30.2	3.9	1014	4	US-09-328-352-1661	Sequence 1661, Ap
C 91	30.2	3.9	72604	3	US-09-268-992-7	Sequence 7, Appli
C 92	30.2	3.9	72604	3	US-09-657-474-7	Sequence 23621, A
C 93	30	3.9	372	4	US-09-513-999C-23621	Sequence 17, Appl
C 94	30	3.9	382	4	US-09-438-906-17	Sequence 8976, Ap
C 95	30	3.9	399	4	US-09-621-976-8976	Sequence 38, Appl
C 96	30	3.9	838	4	US-09-539-333D-38	Sequence 39, Appl
C 97	30	3.9	985	4	US-09-539-333D-39	Sequence 37, Appl
C 98	30	3.9	1154	4	US-09-539-333D-37	Sequence 874, App
C 99	30	3.9	1236	4	US-09-134-000C-874	Sequence 36, Appl
C 100	30	3.9	1301	4	US-09-539-333D-36	

101	30	3.9	1357	4	US-09-461-325-55	Sequence 55, Appl	174	29.2	3.8	2498	4	US-09-620-312D-90	Sequence 90, Appl
102	30	3.9	1357	4	US-10-012-542-55	Sequence 55, Appl	175	29.2	3.8	2920	4	US-09-620-312D-1084	Sequence 1084, Ap
103	30	3.9	1357	4	US-10-115-123-55	Sequence 55, Appl	C 176	29.2	3.8	3522	4	US-09-248-796A-5210	Sequence 5210, Ap
C 104	30	3.9	1386	4	US-09-539-333D-40	Sequence 40, Appl	C 177	29.2	3.8	75395	4	US-09-984-890-3	Sequence 3, Appli
C 105	30	3.9	1902	4	US-09-583-110-1360	Sequence 1360, Ap	C 178	29.2	3.8	75395	4	US-10-274-194-3	Sequence 3, Appli
C 106	30	3.9	2007	4	US-09-328-352-2460	Sequence 2460, Ap	C 179	29	3.8	986	4	US-09-270-767-14027	Sequence 14027, A
C 107	30	3.9	8148	4	US-08-961-527-11	Sequence 11, Appl	C 180	29	3.8	1200	4	US-09-248-796A-4154	Sequence 4154, Ap
C 108	30	3.9	319608	4	US-09-539-333D-1	Sequence 1, Appli	C 181	29	3.8	1329	4	US-09-787-083-5	Sequence 5, Appli
C 109	30	3.9	319608	4	US-09-679-409-1	Sequence 1, Appli	C 182	29	3.8	1359	4	US-09-248-796A-6193	Sequence 6193, Ap
C 110	29.8	3.9	298	4	US-09-313-294A-7544	Sequence 7544, Ap	C 183	29	3.8	1548	4	US-09-248-796A-4161	Sequence 4161, Ap
C 111	29.8	3.9	567	3	US-09-385-982-427	Sequence 427, App	C 184	29	3.8	1587	4	US-09-614-221A-202	Sequence 202, App
C 112	29.8	3.9	698	4	US-09-270-767-9087	Sequence 9087, Ap	C 185	29	3.8	1609	4	US-09-620-312D-8	Sequence 8, Appli
C 113	29.8	3.9	698	4	US-09-270-767-24369	Sequence 24369, A	C 186	29	3.8	1884	4	US-10-246-658-3	Sequence 3, Appli
C 114	29.8	3.9	704	4	US-09-023-655-46	Sequence 46, Appl	C 187	29	3.8	2013	4	US-09-292-858B-1	Sequence 1, Appli
C 115	29.8	3.9	1152	1	US-08-315-831A-13	Sequence 13, Appl	C 188	29	3.8	2058	4	US-10-246-658-1	Sequence 1, Appli
C 116	29.8	3.9	1152	1	US-08-662-318-13	Sequence 13, Appl	C 189	29	3.8	2652	2	US-08-366-547-1	Sequence 1, Appli
C 117	29.8	3.9	1152	5	PCT-US95-12509-13	Sequence 13, Appl	C 190	29	3.8	3001	4	US-09-539-333D-226	Sequence 226, App
C 118	29.8	3.9	1316	1	US-07-755-461A-12	Sequence 12, Appl	C 191	29	3.8	9048	3	US-08-973-273-4	Sequence 4, Appli
C 119	29.8	3.9	1316	1	US-08-315-831A-12	Sequence 12, Appl	C 192	28.8	3.8	250	4	US-09-513-999C-32028	Sequence 32028, A
C 120	29.8	3.9	1316	1	US-08-662-318-12	Sequence 12, Appl	C 193	28.8	3.8	637	4	US-09-270-767-4501	Sequence 4501, Ap
C 121	29.8	3.9	1316	5	PCT-US95-12509-12	Sequence 12, Appl	C 194	28.8	3.8	637	4	US-09-270-767-19783	Sequence 19783, A
C 122	29.8	3.9	1430	4	US-09-016-434-710	Sequence 710, App	C 195	28.8	3.8	802	4	US-09-311-021-87	Sequence 87, Appl
C 123	29.8	3.9	4608	1	US-07-718-575-11	Sequence 11, Appl	C 196	28.8	3.8	804	4	US-09-149-476-125	Sequence 125, App
C 124	29.8	3.9	4608	1	US-08-481-206-11	Sequence 11, Appl	C 197	28.8	3.8	930	4	US-08-956-171E-813	Sequence 813, App
C 125	29.8	3.9	4608	2	US-08-486-269A-11	Sequence 11, Appl	C 198	28.8	3.8	930	4	US-08-781-986A-813	Sequence 813, App
C 126	29.8	3.9	112132	4	US-09-741-150-3	Sequence 3, Appli	C 199	28.8	3.8	1320	4	US-09-149-476-278	Sequence 278, App
C 127	29.8	3.9	112132	4	US-10-160-187-3	Sequence 3, Appli	C 200	28.8	3.8	1808	1	US-08-351-149-4	Sequence 4, Appli
C 128	29.8	3.9	1830121	4	US-09-557-884-1	Sequence 1, Appli	C 201	28.8	3.8	1808	1	US-08-384-828-4	Sequence 4, Appli
C 129	29.8	3.9	1830121	4	US-09-643-990A-1	Sequence 1, Appli	C 202	28.8	3.8	1808	3	US-08-895-474-4	Sequence 4, Appli
C 130	29.8	3.9	1830121	4	US-10-329-960-1	Sequence 1, Appli	C 203	28.8	3.8	1859	3	US-07-861-458C-1	Sequence 1, Appli
C 131	29.6	3.9	400	1	US-08-208-08C-1	Sequence 1, Appli	C 204	28.8	3.8	1970	4	US-09-311-021-41	Sequence 41, Appl
C 132	29.6	3.9	500	4	US-09-270-767-9290	Sequence 9290, Ap	C 205	28.8	3.8	2748	3	US-09-199-290-33	Sequence 33, Appl
C 133	29.6	3.9	500	4	US-09-270-767-24572	Sequence 24572, A	C 206	28.8	3.8	2748	4	US-09-821-616-33	Sequence 33, Appl
C 134	29.6	3.9	834	4	US-09-328-352-3810	Sequence 3810, Ap	C 207	28.8	3.8	3075	4	US-09-799-451-32	Sequence 32, Appl
C 135	29.6	3.9	1449	4	US-09-248-796A-3697	Sequence 3697, Ap	C 208	28.8	3.8	3275	4	US-09-370-838-151	Sequence 151, App
C 136	29.6	3.9	1565	3	US-08-468-846-1	Sequence 1, Appli	C 209	28.8	3.8	3275	4	US-09-854-133-151	Sequence 151, App
C 137	29.6	3.9	1565	3	US-08-915-096A-1	Sequence 1, Appli	C 210	28.8	3.8	4407	5	PCT-US93-05701-1	Sequence 1, Appli
C 138	29.6	3.9	1672	4	US-09-023-655-1472	Sequence 1472, Ap	C 211	28.8	3.8	5610	4	US-10-204-708-53	Sequence 53, Appl
C 139	29.6	3.9	3288	1	US-08-208-08C-3	Sequence 3, Appli	C 212	28.8	3.8	5910	1	US-08-195-814-1	Sequence 1, Appli
C 140	29.6	3.9	5150	3	US-09-068-140A-14	Sequence 14, Appl	C 213	28.8	3.8	6405	4	US-08-961-527-107	Sequence 107, App
C 141	29.6	3.9	9578	4	US-08-961-527-127	Sequence 127, App	C 214	28.6	3.7	506	3	US-08-916-576B-10	Sequence 10, Appl
C 142	29.6	3.9	22846	2	US-08-469-461-3	Sequence 3, Appli	C 215	28.6	3.7	570	4	US-09-248-796A-5338	Sequence 5338, Ap
C 143	29.6	3.9	22846	3	US-07-890-609-3	Sequence 3, Appli	C 216	28.6	3.7	618	3	US-09-385-982-24	Sequence 24, Appl
C 144	29.6	3.9	1664976	4	US-08-916-421B-1	Sequence 1, Appli	C 217	28.6	3.7	885	4	US-09-583-110-528	Sequence 528, App
C 145	29.6	3.9	1664976	4	US-09-692-570-1	Sequence 1, Appli	C 218	28.6	3.7	1081	4	US-09-016-434-928	Sequence 928, App
C 146	29.6	3.9	1830121	4	US-09-557-884-1	Sequence 1, Appli	C 219	28.6	3.7	1173	3	US-08-993-380-3	Sequence 3, Appli
C 147	29.6	3.9	1830121	4	US-09-643-990A-1	Sequence 1, Appli	C 220	28.6	3.7	1399	3	US-09-049-698-17	Sequence 17, Appl
C 148	29.6	3.9	1830121	4	US-10-329-960-1	Sequence 1, Appli	C 221	28.6	3.7	1575	3	US-08-639-294-1	Sequence 1, Appli
C 149	29.4	3.8	365	4	US-09-621-976-8348	Sequence 8348, Ap	C 222	28.6	3.7	1575	4	US-09-861-034B-1	Sequence 1, Appli
C 150	29.4	3.8	420	4	US-09-134-000C-2341	Sequence 2341, Ap	C 223	28.6	3.7	1764	3	US-09-013-881-13	Sequence 13, Appl
C 151	29.4	3.8	433	4	US-09-513-999C-24898	Sequence 24898, A	C 224	28.6	3.7	1764	4	US-09-612-473-13	Sequence 13, Appl
C 152	29.4	3.8	909	4	US-09-248-796A-3116	Sequence 3116, Ap	C 225	28.6	3.7	1915	3	US-09-147-915-1	Sequence 1, Appli
C 153	29.4	3.8	1419	4	US-09-248-796A-12098	Sequence 12098, A	C 226	28.6	3.7	1926	4	US-09-270-767-27574	Sequence 27574, A
C 154	29.4	3.8	2598	4	US-09-248-796A-3589	Sequence 3589, Ap	C 227	28.6	3.7	2016	1	US-08-294-872-1	Sequence 1, Appli
C 155	29.4	3.8	4002	2	US-08-540-804-11	Sequence 11, Appl	C 228	28.6	3.7	2016	5	PCT-US95-09823-1	Sequence 1, Appli
C 156	29.4	3.8	4002	2	US-08-218-265-11	Sequence 11, Appl	C 229	28.6	3.7	2661	4	US-09-248-796A-3901	Sequence 3901, Ap
C 157	29.4	3.8	4002	3	US-08-521-872-11	Sequence 11, Appl	C 230	28.6	3.7	2933	3	US-08-936-165A-201	Sequence 201, App
C 158	29.4	3.8	4002	3	US-08-590-399-11	Sequence 11, Appl	C 231	28.6	3.7	2943	4	US-09-503-922-2	Sequence 2, Appli
C 159	29.4	3.8	4631	4	US-09-799-451-394	Sequence 394, App	C 232	28.6	3.7	3018	2	US-08-860-150-6	Sequence 6, Appli
C 160	29.4	3.8	4822	4	US-09-270-767-12784	Sequence 12784, A	C 233	28.6	3.7	3043	3	US-09-338-132-6	Sequence 6, Appli
C 161	29.4	3.8	29793	3	US-09-302-812-38	Sequence 38, Appl	C 234	28.6	3.7	3043	3	US-09-049-698-16	Sequence 16, Appl
C 162	29.4	3.8	29793	3	US-09-511-477-38	Sequence 38, Appl	C 235	28.6	3.7	3181	3	US-09-049-698-18	Sequence 18, Appl
C 163	29.4	3.8	29793	3	US-09-511-507-38	Sequence 38, Appl	C 236	28.6	3.7	3454	4	US-09-270-767-11909	Sequence 11909, A
C 164	29.4	3.8	1230025	4	US-09-198-452A-1	Sequence 1, Appli	C 237	28.6	3.7	4330	3	US-09-310-293-1	Sequence 1, Appli
C 165	29.4	3.8	1664976	4	US-08-916-421B-1	Sequence 1, Appli	C 238	28.6	3.7	4330	3	US-09-579-376-1	Sequence 1, Appli
C 166	29.4	3.8	1664976	4	US-09-692-570-1	Sequence 1, Appli	C 239	28.6	3.7	4673	1	US-07-638-431-1	Sequence 1, Appli
C 167	29.2	3.8	216	1	US-08-686-878A-34	Sequence 34, Appl	C 240	28.6	3.7	4673	5	PCT-US92-00018-1	Sequence 1, Appli
C 168	29.2	3.8	216	3	US-09-175-928-34	Sequence 34, Appl	C 241	28.6	3.7	11873	2	US-08-970-269A-32	Sequence 32, Appl
C 169	29.2	3.8	456	4	US-09-248-796A-14094	Sequence 14094, A	C 242	28.6	3.7	11873	3	US-09-407-562-32	Sequence 32, Appl
C 170	29.2	3.8	1011	4	US-09-248-796A-3838	Sequence 3838, Ap	C 243	28.6	3.7	11878	2	US-08-970-269A-31	Sequence 31, Appl
C 171	29.2	3.8	1477	4	US-09-560-761-27	Sequence 27, Appl	C 244	28.6	3.7	11878	3	US-09-407-562-31	Sequence 31, Appl
C 172	29.2	3.8	1747	4	US-09-244-805-23	Sequence 23, Appl	C 245	28.6	3.7	11883	2	US-08-970-269A-28	Sequence 28, Appl
C 173	29.2	3.8	2229	4	US-09-774-528-283	Sequence 283, App	C 246	28.6	3.7	11883	3	US-09-407-562-28	Sequence 28, Appl

C 247	28.6	3.7	14051	4	US-08-956-171E-103	Sequence 103, App	C 320	28.2	3.7	2237	4	US-09-148-545-104	Sequence 104, App
C 248	28.6	3.7	14051	4	US-08-781-986A-103	Sequence 103, App	321	28.2	3.7	2577	4	US-09-952-060-1	Sequence 1, Appli
C 249	28.4	3.7	200	4	US-09-688-990-11	Sequence 11, Appl	322	28.2	3.7	2577	4	US-09-952-060-3	Sequence 3, Appli
250	28.4	3.7	219	1	US-08-702-080-3	Sequence 3, Appli	323	28.2	3.7	2650	4	US-09-952-060-5	Sequence 5, Appli
251	28.4	3.7	219	2	US-08-858-830-3	Sequence 3, Appli	324	28.2	3.7	2650	4	US-09-952-060-7	Sequence 7, Appli
252	28.4	3.7	219	2	US-08-858-834-3	Sequence 3, Appli	325	28.2	3.7	2659	4	US-09-148-545-42	Sequence 42, Appl
C 253	28.4	3.7	242	3	US-09-049-698-11	Sequence 11, Appl	326	28.2	3.7	3857	4	US-09-976-594-915	Sequence 915, App
254	28.4	3.7	264	4	US-09-556-877-274	Sequence 274, App	327	28.2	3.7	3887	4	US-09-976-594-660	Sequence 660, App
255	28.4	3.7	264	4	US-09-620-412C-274	Sequence 274, App	328	28.2	3.7	4053	4	US-09-952-060-34	Sequence 34, Appl
256	28.4	3.7	264	4	US-09-598-419-274	Sequence 274, App	329	28.2	3.7	4053	4	US-09-221-017B-835	Sequence 835, App
C 257	28.4	3.7	264	4	US-09-248-796A-12744	Sequence 12744, A	C 330	28.2	3.7	3630	4	US-08-206-176-5	Sequence 5, Appli
258	28.4	3.7	301	4	US-09-270-767-5573	Sequence 5573, Ap	331	28.2	3.7	10564	1	US-08-206-176-5	Sequence 5, Appli
259	28.4	3.7	301	4	US-09-270-767-20855	Sequence 20855, A	C 332	28.2	3.7	10592	1	US-08-680-726A-51	Sequence 51, Appl
C 260	28.4	3.7	355	4	US-09-513-999C-1174	Sequence 1174, Ap	C 333	28.2	3.7	10592	1	US-08-680-726A-52	Sequence 52, Appl
C 261	28.4	3.7	432	4	US-09-248-796A-7360	Sequence 7360, Ap	C 334	28.2	3.7	10592	3	US-09-092-409-51	Sequence 51, Appl
C 262	28.4	3.7	469	3	US-09-222-575-128	Sequence 128, App	C 335	28.2	3.7	10592	3	US-09-092-409-52	Sequence 52, Appl
C 263	28.4	3.7	469	4	US-09-389-681-128	Sequence 128, App	C 336	28.2	3.7	15378	3	US-08-785-420-1	Sequence 1, Appli
C 264	28.4	3.7	469	4	US-09-620-405B-128	Sequence 128, App	337	28.2	3.7	38519	4	US-09-952-060-28	Sequence 28, Appl
C 265	28.4	3.7	469	4	US-09-339-338-128	Sequence 128, App	337	28.2	3.7	84495	3	US-09-797-906-3	Sequence 3, Appli
C 266	28.4	3.7	469	4	US-09-433-826B-128	Sequence 128, App	338	28.2	3.7	92139	4	US-09-918-686-1	Sequence 1, Appli
C 267	28.4	3.7	469	4	US-09-604-287A-128	Sequence 128, App	C 339	28.2	3.7	1230025	4	US-09-198-452A-1	Sequence 1, Appli
C 268	28.4	3.7	469	4	US-09-285-480-128	Sequence 128, App	340	28	3.7	312	3	US-08-746-160-8	Sequence 8, Appli
C 269	28.4	3.7	469	4	US-09-834-759-128	Sequence 128, App	341	28	3.7	312	3	US-08-810-324-5	Sequence 5, Appli
C 270	28.4	3.7	469	4	US-09-590-751A-128	Sequence 128, App	342	28	3.7	360	3	US-08-746-160-2	Sequence 2, Appli
C 271	28.4	3.7	526	4	US-09-621-976-3217	Sequence 3217, Ap	343	28	3.7	360	3	US-08-810-324-2	Sequence 2, Appli
C 272	28.4	3.7	738	4	US-09-248-796A-931	Sequence 931, App	344	28	3.7	381	2	US-08-808-277A-2	Sequence 2, Appli
C 273	28.4	3.7	855	4	US-09-248-796A-10854	Sequence 10854, A	345	28	3.7	387	2	US-08-480-774A-3	Sequence 3, Appli
C 274	28.4	3.7	1128	1	US-08-381-280-4	Sequence 4, Appli	346	28	3.7	389	2	US-08-808-277A-8	Sequence 8, Appli
C 275	28.4	3.7	1128	1	US-08-381-280-9	Sequence 9, Appli	347	28	3.7	438	4	US-09-513-999C-27526	Sequence 27526, A
276	28.4	3.7	1128	2	US-08-445-533-4	Sequence 18, Appl	348	28	3.7	608	3	US-09-385-982-36	Sequence 36, Appl
C 277	28.4	3.7	1128	2	US-08-445-533-9	Sequence 9, Appli	C 350	28	3.7	870	3	US-09-134-001C-80	Sequence 80, Appl
C 278	28.4	3.7	1128	2	US-08-445-533-18	Sequence 18, Appl	C 351	28	3.7	961	4	US-09-671-317-5	Sequence 5, Appli
C 279	28.4	3.7	1128	2	US-09-052-085-4	Sequence 4, Appli	C 352	28	3.7	1134	4	US-10-101-464A-323	Sequence 323, App
C 280	28.4	3.7	1128	3	US-09-052-085-9	Sequence 9, Appli	C 353	28	3.7	1227	4	US-09-248-796A-7521	Sequence 7521, Ap
C 281	28.4	3.7	1128	3	US-09-052-085-18	Sequence 18, Appl	C 354	28	3.7	1420	4	US-09-690-942-11	Sequence 11, Appl
282	28.4	3.7	1188	1	US-08-048-700-1	Sequence 1, Appli	C 355	28	3.7	1422	3	US-08-387-117-8	Sequence 8, Appli
283	28.4	3.7	1188	3	US-08-339-711-5	Sequence 5, Appli	356	28	3.7	1482	4	US-09-252-991A-11453	Sequence 11453, A
284	28.4	3.7	1226	1	US-08-374-686-4	Sequence 4, Appli	C 357	28	3.7	1905	3	US-08-387-117-7	Sequence 7, Appli
C 285	28.4	3.7	1296	4	US-09-134-000C-1947	Sequence 1947, Ap	C 358	28	3.7	2277	1	US-08-676-967-2	Sequence 2, Appli
C 286	28.4	3.7	1349	1	US-08-374-686-1	Sequence 1, Appli	C 359	28	3.7	2277	2	US-09-098-487-2	Sequence 2, Appli
C 287	28.4	3.7	1470	4	US-09-016-434-1203	Sequence 58, Appl	C 360	28	3.7	5102	4	US-09-023-655-1426	Sequence 1426, Ap
C 288	28.4	3.7	1588	3	US-08-858-207A-58	Sequence 1203, Ap	C 361	28	3.7	5102	4	US-09-919-497-8	Sequence 8, Appli
C 289	28.4	3.7	1716	4	US-09-710-279-117	Sequence 117, App	C 362	28	3.7	7141	4	US-09-631-594-73	Sequence 73, Appl
C 290	28.4	3.7	1722	3	US-09-134-001C-2189	Sequence 2189, Ap	C 363	28	3.7	11831	4	US-08-961-527-65	Sequence 65, Appl
C 291	28.4	3.7	1786	4	US-09-976-594-274	Sequence 274, App	C 364	28	3.7	19446	4	US-08-961-527-51	Sequence 51, Appl
292	28.4	3.7	1873	3	US-08-910-864-13	Sequence 13, Appl	365	28	3.7	640681	4	US-09-790-988-1	Sequence 1, Appli
C 293	28.4	3.7	1873	3	US-09-107-532A-2699	Sequence 2699, Ap	366	27.8	3.6	357	4	US-09-513-999C-19160	Sequence 19160, A
C 294	28.4	3.7	3164	4	US-09-710-279-3828	Sequence 3828, Ap	C 367	27.8	3.6	546	4	US-09-543-681A-1765	Sequence 1765, Ap
C 295	28.4	3.7	3234	4	US-09-710-279-3853	Sequence 3853, Ap	368	27.8	3.6	573	4	US-09-248-796A-5065	Sequence 5065, Ap
C 296	28.4	3.7	3475	4	US-09-710-279-4032	Sequence 4032, Ap	369	27.8	3.6	702	4	US-09-472-087-41	Sequence 41, Appl
C 297	28.4	3.7	4301	3	US-08-121-446-3	Sequence 3, Appli	370	27.8	3.6	702	4	US-09-248-796A-298	Sequence 58, Appl
C 298	28.4	3.7	5852	1	US-07-867-106-2	Sequence 2, Appli	C 371	27.8	3.6	873	4	US-09-248-796A-392	Sequence 298, App
C 299	28.4	3.7	50000	3	US-09-146-053-3	Sequence 3, Appli	C 372	27.8	3.6	954	4	US-09-248-796A-432	Sequence 392, App
C 300	28.4	3.7	391	2	US-08-808-277A-10	Sequence 10, Appl	373	27.8	3.6	988	4	US-09-774-528-432	Sequence 432, App
C 301	28.2	3.7	504	3	US-08-965-903B-14	Sequence 14, Appl	374	27.8	3.6	1002	4	US-09-134-000C-2083	Sequence 2083, Ap
C 302	28.2	3.7	546	4	US-09-248-796A-13542	Sequence 13542, A	375	27.8	3.6	1241	4	US-09-737-698B-25	Sequence 25, Appl
C 303	28.2	3.7	782	4	US-09-780-717-31	Sequence 31, Appl	376	27.8	3.6	1241	4	US-09-737-626A-25	Sequence 25, Appl
304	28.2	3.7	789	6	5219739-8	Patent No. 5219739	377	27.8	3.6	1290	4	US-10-251-503-1	Sequence 1, Appli
305	28.2	3.7	975	4	US-09-248-796A-5867	Sequence 5867, Ap	C 378	27.8	3.6	1533	3	US-09-002-285-89	Sequence 89, Appl
C 306	28.2	3.7	1014	4	US-09-325-932A-15	Sequence 15, Appl	C 379	27.8	3.6	1533	4	US-09-589-477-89	Sequence 89, Appl
307	28.2	3.7	1276	4	US-09-673-395A-108	Sequence 108, App	C 380	27.8	3.6	1533	4	US-10-099-285A-89	Sequence 89, Appl
308	28.2	3.7	1278	4	US-09-248-796A-1321	Sequence 1321, Ap	C 381	27.8	3.6	1756	2	US-08-879-260-3	Sequence 3, Appli
309	28.2	3.7	1434	4	US-09-673-395A-113	Sequence 113, App	C 382	27.8	3.6	1788	4	US-09-583-110-1283	Sequence 1283, Ap
310	28.2	3.7	1434	4	US-09-673-395A-551	Sequence 551, App	C 383	27.8	3.6	1811	3	US-09-231-529-5	Sequence 5, Appli
311	28.2	3.7	1452	4	US-09-248-796A-6115	Sequence 6115, Ap	C 384	27.8	3.6	1811	3	US-08-977-816-5	Sequence 5, Appli
312	28.2	3.7	1664	1	US-08-250-740-34	Sequence 34, Appl	385	27.8	3.6	1822	2	US-08-757-046A-2	Sequence 2, Appli
C 313	28.2	3.7	1664	1	US-07-695-472B-3	Sequence 3, Appli	386	27.8	3.6	1822	3	US-09-447-208-2	Sequence 2, Appli
C 314	28.2	3.7	1664	4	US-09-106-375-3	Sequence 3, Appli	387	27.8	3.6	1822	3	US-09-135-988-2	Sequence 2, Appli
C 315	28.2	3.7	1675	4	US-09-854-133-395	Sequence 395, App	388	27.8	3.6	1822	3	US-09-277-716-2	Sequence 2, Appli
316	28.2	3.7	1736	4	US-09-620-312D-540	Sequence 540, App	389	27.8	3.6	1822	3	US-08-597-274A-2	Sequence 2, Appli
317	28.2	3.7	1865	4	US-09-620-312D-539	Sequence 539, App	390	27.8	3.6	1822	4	US-09-908-909-2	Sequence 2, Appli
318	28.2	3.7	2000	4	US-09-705-267A-19	Sequence 19, Appl	391	27.8	3.6	1822	4	US-09-609-161B-2	Sequence 2, Appli
C 319	28.2	3.7					392	27.8	3.6	1822	4	US-08-990-103-2	Sequence 2, Appli

393	27.8	3.6	1822	4	US-09-746-485A-2	Sequence 2, Appli	C 466	27.6	3.6	4210	4	US-09-710-279-3761	Sequence 3761, Ap
394	27.8	3.6	1822	4	US-10-126-139-2	Sequence 2, Appli	C 467	27.6	3.6	5055	3	US-09-242-632A-13	Sequence 13, Appl
395	27.8	3.6	1822	4	US-10-126-798-2	Sequence 2, Appli	C 468	27.6	3.6	5652	4	US-09-601-198-75	Sequence 75, Appl
396	27.8	3.6	1822	4	US-10-126-777-2	Sequence 2, Appli	C 469	27.6	3.6	6156	4	US-09-392-812A-3	Sequence 3, Appli
C 397	27.8	3.6	2268	4	US-09-642-034-4	Sequence 4, Appli	C 470	27.6	3.6	6527	4	US-09-492-308A-3	Sequence 3, Appli
C 398	27.8	3.6	2290	6	5312912-1	Patent No. 5312912	C 471	27.6	3.6	6854	4	US-08-961-527-200	Sequence 200, App
C 399	27.8	3.6	2364	4	US-09-307-106-53	Sequence 53, Appl	C 472	27.6	3.6	8961	4	US-10-204-708-79	Sequence 79, Appl
C 400	27.8	3.6	2366	3	US-09-002-285-99	Sequence 99, Appl	C 473	27.6	3.6	16995	4	US-08-961-527-82	Sequence 82, Appl
C 401	27.8	3.6	2366	4	US-09-589-477-99	Sequence 99, Appl	C 474	27.6	3.6	24358	4	US-09-392-812A-1	Sequence 1, Appli
C 402	27.8	3.6	2366	4	US-10-099-285A-99	Sequence 99, Appl	C 475	27.6	3.6	37950	3	US-09-338-907-183	Sequence 183, App
C 403	27.8	3.6	2369	3	US-10-002-285-93	Sequence 93, Appl	C 476	27.6	3.6	37950	3	US-09-218-207-183	Sequence 183, App
C 404	27.8	3.6	2369	4	US-09-589-477-93	Sequence 93, Appl	C 477	27.6	3.6	137000	4	US-10-172-911-11	Sequence 11, Appl
C 405	27.8	3.6	2369	4	US-10-099-285A-93	Sequence 93, Appl	C 478	27.4	3.6	395	4	US-09-621-976-8495	Sequence 8495, Ap
C 406	27.8	3.6	2375	3	US-09-002-285-85	Sequence 85, Appl	C 479	27.4	3.6	432	4	US-09-248-796A-7188	Sequence 7188, Ap
C 407	27.8	3.6	2375	3	US-09-002-285-103	Sequence 103, App	C 480	27.4	3.6	453	4	US-09-270-767-2401	Sequence 2401, Ap
C 408	27.8	3.6	2375	4	US-09-589-477-85	Sequence 85, Appl	C 481	27.4	3.6	453	4	US-09-270-767-17683	Sequence 17683, A
C 409	27.8	3.6	2375	4	US-09-589-477-103	Sequence 103, App	C 482	27.4	3.6	453	4	US-09-248-796A-10616	Sequence 10616, A
C 410	27.8	3.6	2375	4	US-10-099-285A-85	Sequence 85, Appl	C 483	27.4	3.6	609	4	US-09-248-796A-5629	Sequence 5629, Ap
C 411	27.8	3.6	2375	4	US-10-099-285A-103	Sequence 103, App	C 484	27.4	3.6	631	4	US-09-270-767-10068	Sequence 10068, A
C 412	27.8	3.6	3461	4	US-09-642-034-1	Sequence 1, Appli	C 485	27.4	3.6	643	3	US-09-385-982-16	Sequence 16, Appl
C 413	27.8	3.6	7766	4	US-09-125-619-3	Sequence 3, Appli	C 486	27.4	3.6	741	4	US-09-134-000C-780	Sequence 780, App
C 414	27.8	3.6	7766	4	US-10-222-566-3	Sequence 3, Appli	C 487	27.4	3.6	987	4	US-09-509-712B-105	Sequence 105, App
C 415	27.8	3.6	7766	4	US-10-143-024A-3	Sequence 3, Appli	C 488	27.4	3.6	1041	4	US-09-540-236-1282	Sequence 1282, Ap
C 416	27.8	3.6	10970	3	US-08-716-351A-5	Sequence 81, Appl	C 489	27.4	3.6	1329	4	US-09-787-083-1	Sequence 1, Appli
417	27.8	3.6	14231	4	US-08-961-527-81	Sequence 2, Appli	C 490	27.4	3.6	1329	4	US-09-787-083-3	Sequence 3, Appli
C 418	27.8	3.6	15225	2	US-08-892-403A-2	Sequence 2, Appli	C 491	27.4	3.6	1329	4	US-09-787-083-7	Sequence 7, Appli
C 419	27.8	3.6	15225	4	US-09-291-894-2	Sequence 82, Appl	C 492	27.4	3.6	1455	4	US-09-270-767-30203	Sequence 39, Appl
C 420	27.8	3.6	16995	4	US-08-961-527-82	Sequence 3, Appli	C 493	27.4	3.6	1531	3	US-09-347-878-39	Sequence 2, Appli
421	27.8	3.6	38844	3	US-09-734-675-3	Sequence 3, Appli	C 494	27.4	3.6	1758	4	US-09-462-951B-2	Sequence 2, Appli
C 422	27.8	3.6	65042	4	US-09-784-316-3	Sequence 3, Appli	C 495	27.4	3.6	2017	4	US-09-270-767-12457	Sequence 12457, A
C 423	27.8	3.6	65042	4	US-10-229-124-3	Sequence 3, Appli	C 496	27.4	3.6	2187	4	US-09-270-767-14103	Sequence 14103, A
424	27.8	3.6	90050	3	US-09-245-041-5	Sequence 5, Appli	C 497	27.4	3.6	2592	4	US-09-620-312D-301	Sequence 301, App
425	27.8	3.6	90050	4	US-09-358-055B-5	Sequence 5, Appli	C 498	27.4	3.6	4821	3	US-08-913-374-1	Sequence 1, Appli
C 426	27.8	3.6	90050	4	US-09-893-238-5	Sequence 5, Appli	C 499	27.4	3.6	5527	4	US-09-696-115B-1	Sequence 1, Appli
C 427	27.8	3.6	246240	2	US-08-724-394A-20	Sequence 20, Appl	C 500	27.4	3.6	5733	2	US-08-473-553A-1	Sequence 1, Appli
C 428	27.8	3.6	246240	2	US-08-724-394A-21	Sequence 21, Appl	C 501	27.4	3.6	6669	4	US-10-204-708-6	Sequence 6, Appli
C 429	27.8	3.6	246240	2	US-08-724-394A-22	Sequence 22, Appl	C 502	27.4	3.6	7304	4	US-10-204-708-44	Sequence 44, Appl
C 430	27.6	3.6	187	4	US-09-621-976-13418	Sequence 13418, A	C 503	27.4	3.6	7585	4	US-09-418-710-22	Sequence 22, Appl
C 431	27.6	3.6	261	4	US-09-248-796A-11472	Sequence 11472, A	C 504	27.4	3.6	7585	4	US-09-839-479-22	Sequence 22, Appl
C 432	27.6	3.6	273	4	US-09-270-767-6188	Sequence 6188, Ap	C 505	27.4	3.6	7995	4	US-09-821-726A-11	Sequence 11, Appl
C 433	27.6	3.6	273	4	US-09-270-767-21470	Sequence 21470, A	C 506	27.4	3.6	8959	1	US-08-920-812-1	Sequence 1, Appli
C 434	27.6	3.6	291	4	US-09-583-110-928	Sequence 928, App	C 507	27.4	3.6	8959	1	US-08-920-827-1	Sequence 1, Appli
C 435	27.6	3.6	302	4	US-09-621-976-16091	Sequence 16091, A	C 508	27.4	3.6	8959	1	US-08-921-177-1	Sequence 1, Appli
C 436	27.6	3.6	324	4	US-09-513-999C-2028	Sequence 2028, Ap	C 509	27.4	3.6	8959	1	US-08-362-577C-1	Sequence 1, Appli
C 437	27.6	3.6	339	4	US-09-248-796A-5971	Sequence 5971, Ap	C 510	27.4	3.6	8959	2	US-08-920-828-1	Sequence 1, Appli
C 438	27.6	3.6	345	4	US-09-248-796A-7481	Sequence 7481, Ap	C 511	27.4	3.6	9060	3	US-08-378-313-20	Sequence 20, Appl
C 439	27.6	3.6	490	4	US-09-430-470-5	Sequence 5, Appli	C 512	27.4	3.6	12127	4	US-08-961-527-148	Sequence 148, App
C 440	27.6	3.6	493	4	US-09-430-470-9	Sequence 9, Appli	C 513	27.4	3.6	13059	4	US-08-956-171E-220	Sequence 220, App
C 441	27.6	3.6	496	4	US-09-430-470-7	Sequence 7, Appli	C 514	27.4	3.6	13059	4	US-08-781-986A-220	Sequence 220, App
C 442	27.6	3.6	499	4	US-09-430-470-3	Sequence 3, Appli	C 515	27.4	3.6	15572	4	US-09-424-783-1	Sequence 1, Appli
C 443	27.6	3.6	618	4	US-09-134-000C-709	Sequence 709, App	C 516	27.4	3.6	92407	4	US-09-596-002-36	Sequence 36, Appl
C 444	27.6	3.6	618	4	US-09-134-000C-2782	Sequence 2782, Ap	C 517	27.4	3.6	148567	4	US-09-801-876B-3	Sequence 3, Appli
C 445	27.6	3.6	836	4	US-08-961-309-63	Sequence 63, Appl	C 518	27.4	3.6	148567	4	US-10-254-869-3	Sequence 2, Appli
C 446	27.6	3.6	945	4	US-09-583-110-392	Sequence 392, App	C 519	27.4	3.6	4403765	3	US-09-103-840A-2	Sequence 1, Appli
C 447	27.6	3.6	1014	4	US-09-107-532A-2344	Sequence 2344, Ap	C 520	27.4	3.6	4411529	3	US-09-103-840A-1	Sequence 1, Appli
C 448	27.6	3.6	1362	4	US-09-543-681A-3528	Sequence 3528, Ap	C 521	27.2	3.6	270	4	US-09-621-976-16092	Sequence 16092, A
C 449	27.6	3.6	1449	4	US-09-634-238-36	Sequence 36, Appl	C 522	27.2	3.6	275	4	US-09-513-999C-23513	Sequence 23513, A
C 450	27.6	3.6	1632	4	US-09-248-796A-6825	Sequence 6825, Ap	C 523	27.2	3.6	282	4	US-09-248-796A-9539	Sequence 9539, Ap
451	27.6	3.6	1660	4	US-09-270-767-158	Sequence 158, App	C 524	27.2	3.6	285	4	US-09-313-294A-5273	Sequence 5273, Ap
452	27.6	3.6	1660	4	US-09-270-767-1540	Sequence 1540, A	C 525	27.2	3.6	516	4	US-09-248-796A-10405	Sequence 10405, A
453	27.6	3.6	1664	4	US-09-438-917-5	Sequence 5, Appli	C 526	27.2	3.6	519	4	US-09-248-796A-5916	Sequence 5916, Ap
C 454	27.6	3.6	1827	3	US-09-315-793-21	Sequence 21, Appl	C 527	27.2	3.6	655	4	US-09-288-143-20	Sequence 20, Appl
C 455	27.6	3.6	2160	2	US-08-840-236-2	Sequence 2, Appli	C 528	27.2	3.6	687	4	US-09-328-352-1650	Sequence 1650, Ap
C 456	27.6	3.6	2160	2	US-08-840-236-5	Sequence 5, Appli	C 529	27.2	3.6	932	4	US-09-270-767-14999	Sequence 14999, A
C 457	27.6	3.6	2160	2	US-08-505-448A-2	Sequence 2, Appli	C 530	27.2	3.6	951	4	US-09-107-532A-940	Sequence 940, App
C 458	27.6	3.6	2160	2	US-08-505-448A-5	Sequence 5, Appli	C 531	27.2	3.6	975	4	US-09-710-279-2673	Sequence 2673, Ap
C 459	27.6	3.6	2169	4	US-09-434-408-3	Sequence 3, Appli	C 532	27.2	3.6	1188	4	US-09-248-796A-6299	Sequence 6299, Ap
C 460	27.6	3.6	2375	3	US-09-002-285-83	Sequence 83, Appl	C 533	27.2	3.6	1287	3	US-09-134-001C-2042	Sequence 2042, Ap
C 461	27.6	3.6	2375	4	US-09-589-477-83	Sequence 83, Appl	C 534	27.2	3.6	1557	4	US-09-710-279-505	Sequence 505, App
C 462	27.6	3.6	2375	4	US-10-099-285A-83	Sequence 83, Appl	C 535	27.2	3.6	1584	3	US-09-134-001C-1628	Sequence 1628, Ap
C 463	27.6	3.6	2906	3	US-09-453-702B-186	Sequence 186, App	C 536	27.2	3.6	1700	3	US-08-897-340-4	Sequence 4, Appli
C 464	27.6	3.6	3467	3	US-09-298-924-3	Sequence 3, Appli	C 537	27.2	3.6	1700	3	US-09-252-329-4	Sequence 4, Appli
C 465	27.6	3.6	3592	2	US-08-469-537A-100	Sequence 100, App	C 538	27.2	3.6	1722	4	US-09-248-796A-1650	Sequence 1650, Ap

c 539	27.2	3.6	1730	4	US-09-675-018B-5	Sequence 5, Appli	612	27	3.5	1853	4	US-09-685-166A-369	Sequence 369, App
c 540	27.2	3.6	1854	4	US-09-620-312D-793	Sequence 793, Appl	613	27	3.5	1853	4	US-09-429-755-295	Sequence 295, App
541	27.2	3.6	1923	4	US-09-149-476-192	Sequence 192, App	614	27	3.5	1853	4	US-09-679-426-369	Sequence 369, App
542	27.2	3.6	1988	4	US-09-643-597-173	Sequence 173, App	c 615	27	3.5	2046	4	US-09-543-681A-1281	Sequence 1281, Ap
543	27.2	3.6	1988	4	US-09-480-884A-173	Sequence 173, App	c 616	27	3.5	2079	4	US-09-540-236-830	Sequence 830, App
544	27.2	3.6	1988	4	US-09-542-615A-173	Sequence 173, App	617	27	3.5	2184	3	US-09-439-313-370	Sequence 370, App
545	27.2	3.6	1988	4	US-09-606-421B-173	Sequence 173, App	618	27	3.5	2184	3	US-09-062-451-296	Sequence 296, App
546	27.2	3.6	1988	4	US-09-466-396A-173	Sequence 173, App	619	27	3.5	2184	3	US-09-352-616A-370	Sequence 370, App
547	27.2	3.6	1988	4	US-09-476-496A-173	Sequence 173, App	620	27	3.5	2184	4	US-09-289-198-296	Sequence 296, App
548	27.2	3.6	1988	4	US-09-476-496A-173	Sequence 173, App	621	27	3.5	2184	4	US-09-636-215-370	Sequence 370, App
c 549	27.2	3.6	2049	4	US-09-134-000C-1883	Sequence 1883, Ap	622	27	3.5	2184	4	US-09-685-166A-370	Sequence 370, App
c 550	27.2	3.6	2084	4	US-09-197-970B-2	Sequence 2, Appli	623	27	3.5	2184	4	US-09-429-755-296	Sequence 296, App
551	27.2	3.6	2086	4	US-09-270-767-5329	Sequence 5329, Ap	624	27	3.5	2359	4	US-08-961-527-243	Sequence 243, App
552	27.2	3.6	2086	4	US-09-270-767-5329	Sequence 2086, A	c 625	27	3.5	2682	2	US-08-867-941-7	Sequence 7, Appli
c 553	27.2	3.6	2566	4	US-09-197-970B-1	Sequence 1, Appli	c 626	27	3.5	2682	3	US-09-074-658-7	Sequence 7, Appli
c 554	27.2	3.6	3124	4	US-09-710-279-4128	Sequence 4128, Ap	c 627	27	3.5	2694	2	US-08-867-941-2	Sequence 2, Appli
c 555	27.2	3.6	3202	4	US-09-710-279-3386	Sequence 3386, Ap	c 628	27	3.5	2694	3	US-09-074-658-2	Sequence 2, Appli
c 556	27.2	3.6	3498	4	US-09-200-650E-8	Sequence 8, Appli	c 629	27	3.5	2694	4	US-09-248-796A-1170	Sequence 1170, Ap
c 557	27.2	3.6	3675	4	US-09-107-532A-2566	Sequence 2566, Ap	c 630	27	3.5	2985	4	US-09-710-279-3576	Sequence 3576, Ap
558	27.2	3.6	3842	3	US-09-115-954-7	Sequence 7, Appli	c 631	27	3.5	3043	4	US-09-107-532A-1575	Sequence 1575, Ap
559	27.2	3.6	3912	3	US-09-115-954-1	Sequence 1, Appli	c 632	27	3.5	3135	4	US-09-620-312D-105	Sequence 105, App
c 560	27.2	3.6	4100	4	US-09-620-312D-81	Sequence 81, Appl	c 633	27	3.5	3304	4	US-09-118-442-14	Sequence 14, Appl
561	27.2	3.6	4130	4	US-09-710-279-4126	Sequence 4126, Ap	c 634	27	3.5	3546	3	US-09-118-442-15	Sequence 15, Appl
562	27.2	3.6	4260	4	US-09-635-132-18	Sequence 18, Appl	635	27	3.5	3546	3	US-09-118-442-15	Sequence 15, Appl
c 563	27.2	3.6	4599	1	US-08-431-080-27	Sequence 27, Appl	636	27	3.5	3546	3	US-09-677-064-14	Sequence 14, Appl
c 564	27.2	3.6	4599	2	US-08-938-534-27	Sequence 27, Appl	c 637	27	3.5	3546	3	US-09-677-064-15	Sequence 15, Appl
c 565	27.2	3.6	4599	3	US-09-345-294-27	Sequence 27, Appl	c 638	27	3.5	3600	3	US-08-894-731-1	Sequence 1, Appli
c 566	27.2	3.6	5538	2	US-08-231-193A-55	Sequence 55, Appl	c 639	27	3.5	3636	3	US-09-090-535-5	Sequence 5, Appli
c 567	27.2	3.6	5538	2	US-08-486-273A-55	Sequence 55, Appl	c 640	27	3.5	3636	3	US-09-090-535-6	Sequence 6, Appli
c 568	27.2	3.6	5538	3	US-08-940-086A-55	Sequence 55, Appl	c 641	27	3.5	3636	3	US-09-090-535-7	Sequence 7, Appli
c 569	27.2	3.6	5538	3	US-08-940-035A-55	Sequence 55, Appl	c 642	27	3.5	3636	3	US-09-090-535-8	Sequence 8, Appli
c 570	27.2	3.6	5538	3	US-08-935-105A-55	Sequence 55, Appl	c 643	27	3.5	3997	4	US-09-270-767-28607	Sequence 28607, A
c 571	27.2	3.6	5538	4	US-09-648-797-55	Sequence 55, Appl	c 644	27	3.5	4689	4	US-09-895-652A-10	Sequence 10, Appl
c 572	27.2	3.6	5892	4	US-09-386-123-55	Sequence 55, Appl	c 645	27	3.5	4770	4	US-09-543-681A-826	Sequence 826, App
573	27.2	3.6	5915	4	US-09-583-110-2582	Sequence 55, Appl	c 646	27	3.5	5362	2	US-08-853-310-3	Sequence 3, Appli
574	27.2	3.6	5915	4	US-10-204-708-78	Sequence 78, Appl	647	27	3.5	5421	4	US-09-814-915A-66	Sequence 66, Appl
c 575	27.2	3.6	5983	3	US-08-264-578-1	Sequence 1, Appli	c 648	27	3.5	7641	2	US-08-867-941-6	Sequence 6, Appli
576	27.2	3.6	20303	1	US-08-370-975B-6	Sequence 6, Appli	c 649	27	3.5	7641	3	US-09-074-658-6	Sequence 6, Appli
577	27.2	3.6	25464	4	US-09-326-480A-4	Sequence 4, Appli	c 650	27	3.5	7650	2	US-08-867-941-1	Sequence 1, Appli
578	27.2	3.6	26764	1	US-08-370-975B-1	Sequence 1, Appli	c 651	27	3.5	7650	3	US-09-074-658-1	Sequence 1, Appli
579	27.2	3.6	112132	4	US-09-741-150-3	Sequence 3, Appli	c 652	27	3.5	11049	4	US-10-204-708-22	Sequence 22, Appl
c 580	27.2	3.6	112132	4	US-10-160-187-3	Sequence 3, Appli	c 653	27	3.5	19011	1	US-08-310-356-36	Sequence 36, Appl
c 581	27.2	3.6	168575	4	US-09-426-290-1	Sequence 1, Appli	c 654	27	3.5	19557	5	PCT-US92-06300-1	Sequence 1, Appli
582	27.2	3.6	169998	4	US-09-676-610B-24	Sequence 24, Appl	655	27	3.5	38564	4	US-09-734-673-3	Sequence 3, Appli
583	27.2	3.6	197496	4	US-09-877-177A-10	Sequence 10, Appl	656	27	3.5	53332	4	US-09-801-861-3	Sequence 3, Appli
c 584	27.2	3.6	202001	4	US-09-734-674-3	Sequence 3, Appli	657	27	3.5	53332	4	US-10-224-562-3	Sequence 3, Appli
c 585	27.2	3.6	786431	4	US-09-751-389-3	Sequence 3, Appli	658	27	3.5	55827	4	US-09-813-133A-3	Sequence 3, Appli
c 586	27	3.5	323	4	US-09-270-767-7062	Sequence 7062, Ap	659	27	3.5	319608	4	US-09-539-333D-1	Sequence 1, Appli
c 587	27	3.5	323	4	US-09-270-767-22344	Sequence 22344, A	c 660	27	3.5	392000	4	US-10-027-983-11	Sequence 11, Appl
588	27	3.5	385	4	US-09-621-976-9028	Sequence 9028, Ap	c 661	26.8	3.5	192	4	US-09-248-796A-8980	Sequence 8980, Ap
589	27	3.5	402	4	US-09-270-767-8087	Sequence 8087, Ap	c 662	26.8	3.5	296	4	US-09-023-655-349	Sequence 349, App
590	27	3.5	402	4	US-09-270-767-23369	Sequence 23369, A	c 663	26.8	3.5	303	4	US-09-513-999C-2162	Sequence 2162, Ap
c 591	27	3.5	438	4	US-09-134-000C-607	Sequence 607, App	c 664	26.8	3.5	330	4	US-09-513-999C-1356	Sequence 1356, Ap
592	27	3.5	546	4	US-09-248-796A-4484	Sequence 4484, Ap	c 665	26.8	3.5	474	4	US-09-621-976-18033	Sequence 18033, A
c 593	27	3.5	574	4	US-09-221-017B-370	Sequence 370, App	c 666	26.8	3.5	478	4	US-09-621-976-18425	Sequence 18425, A
c 594	27	3.5	615	4	US-09-854-133-607	Sequence 607, App	667	26.8	3.5	505	4	US-09-621-976-15639	Sequence 15639, A
c 595	27	3.5	885	4	US-09-583-110-1634	Sequence 1634, Ap	668	26.8	3.5	519	4	US-09-107-532A-2906	Sequence 2906, Ap
c 596	27	3.5	1086	4	US-09-543-681A-2888	Sequence 2888, Ap	669	26.8	3.5	581	4	US-09-270-767-7439	Sequence 7439, Ap
597	27	3.5	1283	1	US-07-885-970A-17	Sequence 17, Appl	670	26.8	3.5	581	4	US-09-270-767-22721	Sequence 22721, A
598	27	3.5	1283	1	US-08-298-687A-17	Sequence 17, Appl	c 671	26.8	3.5	585	4	US-09-543-681A-2563	Sequence 2563, Ap
599	27	3.5	1283	1	US-08-530-797-18	Sequence 18, Appl	c 672	26.8	3.5	747	4	US-09-248-796A-4877	Sequence 4877, Ap
600	27	3.5	1283	1	US-08-298-829-17	Sequence 17, Appl	c 673	26.8	3.5	804	3	US-09-134-001C-387	Sequence 387, App
601	27	3.5	1283	2	US-08-787-335-18	Sequence 18, Appl	c 674	26.8	3.5	804	4	US-09-134-000C-2801	Sequence 2801, Ap
c 602	27	3.5	1338	4	US-09-870-472A-7	Sequence 7, Appli	c 675	26.8	3.5	808	4	US-09-270-767-7839	Sequence 7839, Ap
603	27	3.5	1462	4	US-09-672-749-12	Sequence 12, Appl	c 676	26.8	3.5	808	4	US-09-270-767-23121	Sequence 23121, A
c 604	27	3.5	1569	2	US-08-743-637B-176	Sequence 176, App	c 677	26.8	3.5	847	4	US-09-270-767-4112	Sequence 4112, Ap
c 605	27	3.5	1569	3	US-08-526-840B-176	Sequence 176, App	c 678	26.8	3.5	847	4	US-09-270-767-19394	Sequence 19394, A
606	27	3.5	1686	4	US-09-356-806-41	Sequence 41, Appl	c 679	26.8	3.5	887	4	US-09-270-767-11609	Sequence 11609, A
607	27	3.5	1853	3	US-09-439-313-369	Sequence 369, App	c 680	26.8	3.5	909	3	US-08-839-711-2	Sequence 2, Appli
608	27	3.5	1853	3	US-09-062-451-295	Sequence 295, App	681	26.8	3.5	984	3	US-09-277-565-12	Sequence 12, Appl
609	27	3.5	1853	3	US-09-352-616A-369	Sequence 369, App	c 682	26.8	3.5	1308	4	US-09-710-279-3185	Sequence 3185, Ap
610	27	3.5	1853	4	US-09-289-198-295	Sequence 295, App	683	26.8	3.5	1320	4	US-09-248-796A-1865	Sequence 1865, Ap
611	27	3.5	1853	4	US-09-636-215-369	Sequence 369, App	c 684	26.8	3.5	1392	3	US-09-134-001C-1323	Sequence 1323, Ap

C 685	26.8	3.5	1407	4	US-09-248-796A-4441	Sequence 4441, Ap	758	26.6	3.5	445	4	US-09-270-767-4196	Sequence 4196, Ap
C 686	26.8	3.5	1551	4	US-09-328-352-1513	Sequence 1513, Ap	759	26.6	3.5	445	4	US-09-270-767-19478	Sequence 19478, A
C 687	26.8	3.5	1629	5	PCT-US91-02560-3	Sequence 3, Appli	760	26.6	3.5	486	3	US-09-522-217-3	Sequence 3, Appli
688	26.8	3.5	1663	4	US-09-023-655-417	Sequence 417, App	761	26.6	3.5	486	4	US-09-223-246-3	Sequence 3, Appli
689	26.8	3.5	1669	3	US-09-461-697-184	Sequence 184, App	762	26.6	3.5	486	4	US-10-295-723-3	Sequence 3, Appli
C 690	26.8	3.5	1716	4	US-09-248-796A-6272	Sequence 6272, Ap	763	26.6	3.5	503	4	US-09-621-976-15705	Sequence 15705, A
691	26.8	3.5	2099	1	US-08-239-849B-25	Sequence 25, Appl	C 764	26.6	3.5	505	4	US-09-621-976-15639	Sequence 15639, A
692	26.8	3.5	2099	2	US-08-142-368A-25	Sequence 25, Appl	C 765	26.6	3.5	510	4	US-09-248-796A-10295	Sequence 10295, A
693	26.8	3.5	2099	3	US-08-967-727-25	Sequence 25, Appl	C 766	26.6	3.5	534	3	US-09-081-180-20	Sequence 20, Appl
694	26.8	3.5	2099	3	US-08-037-230D-25	Sequence 25, Appl	767	26.6	3.5	534	3	US-09-040-786-20	Sequence 20, Appl
695	26.8	3.5	2099	4	US-09-583-850-25	Sequence 25, Appl	C 768	26.6	3.5	574	4	US-09-621-976-16597	Sequence 16597, A
696	26.8	3.5	2099	4	US-09-579-197-25	Sequence 25, Appl	C 769	26.6	3.5	599	4	US-09-270-767-3552	Sequence 3552, Ap
697	26.8	3.5	2099	4	US-09-404-026-25	Sequence 25, Appl	C 770	26.6	3.5	599	4	US-09-270-767-18834	Sequence 18834, A
698	26.8	3.5	2099	4	US-09-312-464-25	Sequence 25, Appl	771	26.6	3.5	669	4	US-09-328-352-2562	Sequence 2562, Ap
699	26.8	3.5	2150	1	US-08-299-849B-24	Sequence 24, Appl	C 772	26.6	3.5	792	4	US-09-134-001C-1165	Sequence 1165, Ap
700	26.8	3.5	2150	2	US-08-142-368A-24	Sequence 24, Appl	C 773	26.6	3.5	993	3	US-09-248-796A-5468	Sequence 5468, Ap
701	26.8	3.5	2150	3	US-08-967-727-24	Sequence 24, Appl	C 774	26.6	3.5	1080	4	US-09-148-796A-11654	Sequence 11654, A
702	26.8	3.5	2150	3	US-08-037-230D-24	Sequence 24, Appl	C 775	26.6	3.5	1100	4	US-08-956-171E-675	Sequence 675, App
703	26.8	3.5	2150	4	US-09-583-850-24	Sequence 24, Appl	C 776	26.6	3.5	1100	4	US-08-781-986A-675	Sequence 675, App
704	26.8	3.5	2150	4	US-09-579-197-24	Sequence 24, Appl	C 777	26.6	3.5	1118	4	US-09-614-912-181	Sequence 181, App
705	26.8	3.5	2150	4	US-09-404-026-24	Sequence 24, Appl	C 778	26.6	3.5	1125	4	US-09-540-236-310	Sequence 310, App
706	26.8	3.5	2150	4	US-09-312-464-24	Sequence 24, Appl	C 779	26.6	3.5	1140	4	US-09-248-796A-8202	Sequence 8202, Ap
C 707	26.8	3.5	2160	1	US-08-700-749A-8	Sequence 8, Appli	780	26.6	3.5	1149	4	US-09-716-129-38	Sequence 38, Appl
C 708	26.8	3.5	2160	3	US-09-020-684-8	Sequence 8, Appli	781	26.6	3.5	1242	1	US-08-252-966B-13	Sequence 13, Appl
C 709	26.8	3.5	2160	3	US-09-020-467-8	Sequence 8, Appli	782	26.6	3.5	1242	4	US-09-248-796A-1333	Sequence 1333, Ap
C 710	26.8	3.5	2160	3	US-09-020-685-8	Sequence 8, Appli	783	26.6	3.5	1262	4	US-09-149-476-266	Sequence 266, App
C 711	26.8	3.5	2160	3	US-09-020-683-8	Sequence 8, Appli	784	26.6	3.5	1365	3	US-09-134-001C-664	Sequence 664, App
C 712	26.8	3.5	2192	4	US-09-855-323-6	Sequence 6, Appli	785	26.6	3.5	1413	4	US-09-543-681A-3722	Sequence 3722, Ap
C 713	26.8	3.5	2294	4	US-09-270-767-10469	Sequence 10469, A	C 786	26.6	3.5	1581	4	US-09-107-532A-3473	Sequence 3473, Ap
714	26.8	3.5	2458	1	US-08-272-255-5	Sequence 5, Appli	C 787	26.6	3.5	1590	4	US-09-248-796A-5687	Sequence 5687, Ap
715	26.8	3.5	2458	5	PCT-US95-08565-5	Sequence 5, Appli	788	26.6	3.5	1927	1	US-08-336-583-1	Sequence 1, Appli
C 716	26.8	3.5	2730	4	US-09-566-921-28	Sequence 28, Appl	789	26.6	3.5	1927	5	PCT-US95-13795-1	Sequence 1, Appli
717	26.8	3.5	2830	4	US-09-221-017B-730	Sequence 730, App	790	26.6	3.5	2000	1	US-08-469-202-25	Sequence 25, Appl
C 718	26.8	3.5	2894	4	US-09-138-277C-4	Sequence 4, Appli	791	26.6	3.5	2000	2	US-08-484-434C-32	Sequence 32, Appl
C 719	26.8	3.5	2968	4	US-09-527-058-6	Sequence 6, Appli	792	26.6	3.5	2000	4	US-09-384-361-32	Sequence 32, Appl
C 720	26.8	3.5	3117	4	US-09-710-279-4005	Sequence 4005, Ap	C 793	26.6	3.5	2040	4	US-09-134-000C-1762	Sequence 1762, Ap
721	26.8	3.5	3238	3	US-08-123-934A-5	Sequence 5, Appli	794	26.6	3.5	2077	4	US-09-510-543-19	Sequence 19, Appl
722	26.8	3.5	3238	4	US-09-874-628-5	Sequence 5, Appli	795	26.6	3.5	2135	3	US-08-965-903B-7	Sequence 7, Appli
723	26.8	3.5	3238	5	PCT-US94-10080-5	Sequence 5, Appli	C 796	26.6	3.5	2149	4	US-10-101-464A-841	Sequence 841, App
724	26.8	3.5	3296	4	US-09-674-826B-3	Sequence 3, Appli	C 797	26.6	3.5	2430	4	US-09-620-312D-176	Sequence 176, App
725	26.8	3.5	3318	4	US-09-134-000C-2731	Sequence 2731, Ap	C 798	26.6	3.5	2560	4	US-09-023-655-1285	Sequence 1285, Ap
C 726	26.8	3.5	3993	3	US-09-167-109-5	Sequence 5, Appli	799	26.6	3.5	2970	3	US-08-974-180-14	Sequence 14, Appl
C 727	26.8	3.5	4043	4	US-09-710-279-3354	Sequence 3354, Ap	C 800	26.6	3.5	3019	4	US-09-710-279-4232	Sequence 4232, Ap
C 728	26.8	3.5	5583	4	US-09-312-283C-372	Sequence 372, App	C 801	26.6	3.5	3176	1	US-08-425-299A-3	Sequence 3, Appli
729	26.8	3.5	6328	3	US-08-913-832A-1	Sequence 1, Appli	C 802	26.6	3.5	3176	2	US-08-486-663A-14	Sequence 14, Appl
730	26.8	3.5	6328	4	US-09-249-181A-1	Sequence 1, Appli	C 803	26.6	3.5	3176	2	US-08-247-904B-13	Sequence 13, Appl
731	26.8	3.5	6328	4	US-09-158-707-1	Sequence 1, Appli	C 804	26.6	3.5	3176	3	US-08-767-942A-14	Sequence 14, Appl
732	26.8	3.5	6475	4	US-09-620-312D-325	Sequence 325, App	C 805	26.6	3.5	3348	4	US-09-710-279-3541	Sequence 3541, Ap
C 733	26.8	3.5	6766	4	US-09-527-058-1	Sequence 1, Appli	806	26.6	3.5	3497	1	US-08-530-950-5	Sequence 5, Appli
734	26.8	3.5	7432	1	US-07-852-260-1	Sequence 1, Appli	807	26.6	3.5	3497	3	US-09-149-879-5	Sequence 5, Appli
735	26.8	3.5	7432	2	US-08-461-503-1	Sequence 1, Appli	808	26.6	3.5	3497	4	US-09-057-009-5	Sequence 5, Appli
736	26.8	3.5	7432	3	US-08-465-250-1	Sequence 1, Appli	809	26.6	3.5	3498	3	US-08-888-429A-5	Sequence 5, Appli
737	26.8	3.5	7664	4	US-10-204-708-84	Sequence 84, Appl	810	26.6	3.5	3498	4	US-09-593-653-5	Sequence 5, Appli
C 738	26.8	3.5	8078	3	US-08-870-126-12	Sequence 12, Appl	C 811	26.6	3.5	3516	4	US-09-489-039A-3127	Sequence 3127, Ap
C 739	26.8	3.5	8078	4	US-09-445-247-12	Sequence 12, Appl	C 812	26.6	3.5	3542	4	US-09-710-279-4459	Sequence 4459, Ap
740	26.8	3.5	8779	4	US-08-956-171E-58	Sequence 58, Appl	813	26.6	3.5	3553	1	US-08-530-950-7	Sequence 7, Appli
741	26.8	3.5	8779	4	US-08-781-986A-58	Sequence 58, Appl	814	26.6	3.5	3553	3	US-09-149-879-7	Sequence 7, Appli
C 742	26.8	3.5	9706	4	US-09-843-250-5	Sequence 3, Appli	815	26.6	3.5	3553	4	US-09-057-009-7	Sequence 7, Appli
C 743	26.8	3.5	9841	4	US-09-843-250-3	Sequence 3, Appli	816	26.6	3.5	3554	3	US-08-888-429A-7	Sequence 7, Appli
C 744	26.8	3.5	12808	4	US-09-843-250-10	Sequence 10, Appl	817	26.6	3.5	3554	4	US-09-593-653-7	Sequence 7, Appli
C 745	26.8	3.5	14462	4	US-09-843-250-9	Sequence 9, Appli	818	26.6	3.5	3576	1	US-08-530-950-9	Sequence 9, Appli
C 746	26.8	3.5	14985	1	US-08-652-972A-6	Sequence 6, Appli	819	26.6	3.5	3576	3	US-09-358-382-1	Sequence 1, Appli
C 747	26.8	3.5	14985	5	PCT-US96-06231A-6	Sequence 6, Appli	820	26.6	3.5	3576	3	US-08-888-429A-9	Sequence 9, Appli
C 748	26.8	3.5	29604	3	US-08-781-891-207	Sequence 207, App	821	26.6	3.5	3576	3	US-09-149-879-9	Sequence 9, Appli
C 749	26.8	3.5	29604	4	US-09-618-166-207	Sequence 207, App	822	26.6	3.5	3576	4	US-09-016-434-1445	Sequence 1445, Ap
C 750	26.6	3.5	189	4	US-09-248-796A-11074	Sequence 11074, A	823	26.6	3.5	3576	4	US-09-057-009-9	Sequence 9, Appli
751	26.6	3.5	228	3	US-09-134-001C-2670	Sequence 2670, Ap	824	26.6	3.5	3576	4	US-09-593-653-9	Sequence 9, Appli
752	26.6	3.5	303	4	US-08-956-171E-3033	Sequence 3033, Ap	825	26.6	3.5	3587	2	US-08-874-186-91	Sequence 91, Appl
C 753	26.6	3.5	303	4	US-08-781-986A-3033	Sequence 3033, Ap	C 826	26.6	3.5	3600	3	US-08-855-910-7	Sequence 7, Appli
754	26.6	3.5	306	4	US-09-248-796A-5114	Sequence 5114, Ap	C 827	26.6	3.5	3848	2	US-08-808-931-14	Sequence 14, Appl
755	26.6	3.5	354	4	US-09-489-039A-2664	Sequence 2664, Ap	C 828	26.6	3.5	3848	3	US-08-808-323-14	Sequence 14, Appl
756	26.6	3.5	411	4	US-09-134-000C-1810	Sequence 1810, Ap	C 829	26.6	3.5	3848	3	US-09-050-603A-14	Sequence 14, Appl
757	26.6	3.5	439	4	US-09-397-787-164	Sequence 164, App	C 830	26.6	3.5	3848	3	US-09-102-420B-14	Sequence 14, Appl

c 831	26.6	3.5	3848	3	US-09-497-698-14	Sequence 14, Appl	904	26.4	3.4	1269	3	US-09-134-001C-1211	Sequence 1211, Ap
832	26.6	3.5	3876	4	US-09-710-279-3895	Sequence 3895, Appl	905	26.4	3.4	1361	4	US-10-017-372E-36	Sequence 36, Appl
c 833	26.6	3.5	3986	4	US-09-710-279-4014	Sequence 4014, Ap	906	26.4	3.4	1361	4	US-10-017-372E-38	Sequence 38, Appl
834	26.6	3.5	4079	4	US-10-164-595-27	Sequence 27, Appl	c 907	26.4	3.4	1425	4	US-09-710-279-945	Sequence 945, App
835	26.6	3.5	4198	3	US-09-586-719-11	Sequence 11, Appl	c 908	26.4	3.4	1458	3	US-09-134-001C-1457	Sequence 1457, Ap
c 836	26.6	3.5	4741	1	US-07-695-472B-4	Sequence 4, Appli	c 909	26.4	3.4	1515	4	US-09-799-451-492	Sequence 492, App
c 837	26.6	3.5	4741	4	US-09-106-375-4	Sequence 4, Appli	c 910	26.4	3.4	1520	4	US-09-865-879-11	Sequence 11, Appl
c 838	26.6	3.5	4742	1	US-08-250-740-35	Sequence 35, Appl	911	26.4	3.4	1557	4	US-09-248-796A-5190	Sequence 5190, Ap
839	26.6	3.5	5111	3	US-09-004-838-118	Sequence 118, App	c 912	26.4	3.4	1565	4	US-09-149-476-134	Sequence 134, App
840	26.6	3.5	5224	2	US-08-874-186-46	Sequence 46, Appl	c 913	26.4	3.4	1605	4	US-09-270-767-10407	Sequence 10407, A
841	26.6	3.5	5857	4	US-09-220-132-79	Sequence 79, Appl	914	26.4	3.4	1901	3	US-09-338-907-181	Sequence 181, App
842	26.6	3.5	6158	4	US-09-799-451-897	Sequence 897, App	915	26.4	3.4	1901	3	US-09-218-207-181	Sequence 181, App
843	26.6	3.5	6470	4	US-09-620-312D-255	Sequence 255, App	c 916	26.4	3.4	2052	4	US-09-543-681A-1231	Sequence 1231, Ap
844	26.6	3.5	7646	4	US-08-956-171E-121	Sequence 121, App	c 917	26.4	3.4	2075	4	US-09-919-497-41	Sequence 41, Appl
845	26.6	3.5	7646	4	US-08-781-986A-121	Sequence 121, App	c 918	26.4	3.4	2141	4	US-09-841-786-11	Sequence 11, Appl
c 846	26.6	3.5	9310	4	US-08-956-171E-316	Sequence 316, App	c 919	26.4	3.4	2252	4	US-09-270-767-14448	Sequence 14448, A
c 847	26.6	3.5	9310	4	US-08-781-986A-316	Sequence 316, App	920	26.4	3.4	2263	4	US-09-825-497A-42	Sequence 42, Appl
848	26.6	3.5	9347	4	US-10-204-708-35	Sequence 35, Appl	921	26.4	3.4	2315	3	US-09-061-769A-1	Sequence 1, Appli
c 849	26.6	3.5	10711	4	US-08-961-527-145	Sequence 145, App	922	26.4	3.4	2322	3	US-09-061-769A-4	Sequence 4, Appli
c 850	26.6	3.5	15363	4	US-08-961-527-139	Sequence 139, App	923	26.4	3.4	2327	3	US-09-061-769A-3	Sequence 3, Appli
851	26.6	3.5	34794	4	US-09-713-678-39	Sequence 39, Appl	c 924	26.4	3.4	2876	3	US-08-840-204-1	Sequence 1, Appli
852	26.6	3.5	34794	4	US-10-002-720-44	Sequence 44, Appl	925	26.4	3.4	2876	3	US-08-840-204-10	Sequence 10, Appl
c 853	26.6	3.5	35828	3	US-09-449-218D-17	Sequence 17, Appl	c 926	26.4	3.4	2876	4	US-09-324-494A-1	Sequence 1, Appli
c 854	26.6	3.5	35828	4	US-09-668-529A-17	Sequence 17, Appl	927	26.4	3.4	2876	4	US-09-324-494A-10	Sequence 10, Appl
c 855	26.6	3.5	35828	4	US-09-668-037A-17	Sequence 17, Appl	c 928	26.4	3.4	2876	4	US-09-023-655-1187	Sequence 1187, Ap
c 856	26.6	3.5	90050	3	US-09-245-041-5	Sequence 5, Appli	929	26.4	3.4	2994	3	US-09-171-337A-3	GENERAL INFORMA
c 857	26.6	3.5	90050	4	US-09-358-055B-5	Sequence 5, Appli	930	26.4	3.4	2994	4	US-09-631-022-3	GENERAL INFORMA
c 858	26.6	3.5	90050	4	US-09-893-238-5	Sequence 5, Appli	931	26.4	3.4	3050	4	US-09-710-279-3815	Sequence 3815, Ap
c 859	26.4	3.4	261	4	US-09-513-999C-10755	Sequence 10755, A	932	26.4	3.4	3050	4	US-09-710-279-4171	Sequence 4171, Ap
c 860	26.4	3.4	309	4	US-09-313-294A-5781	Sequence 5781, Ap	933	26.4	3.4	3263	4	US-09-023-655-336	Sequence 336, App
c 861	26.4	3.4	335	4	US-09-513-999C-14472	Sequence 14472, A	c 934	26.4	3.4	3388	4	US-09-585-173B-35	Sequence 35, Appl
c 862	26.4	3.4	336	3	US-09-134-001C-2471	Sequence 2471, Ap	935	26.4	3.4	3521	4	US-08-200-232-1	Sequence 1, Appli
c 863	26.4	3.4	340	4	US-09-513-999C-14471	Sequence 14471, A	c 936	26.4	3.4	4042	5	PCT-US95-02219-1	Sequence 1, Appli
864	26.4	3.4	351	4	US-09-203-768A-3	Sequence 3, Appli	c 937	26.4	3.4	4042	5	PCT-US95-02219A-1	Sequence 1, Appli
865	26.4	3.4	356	3	US-08-746-160-6	Sequence 6, Appli	938	26.4	3.4	4233	4	US-09-602-628-9	Sequence 9, Appli
866	26.4	3.4	356	3	US-08-810-324-4	Sequence 4, Appli	939	26.4	3.4	4233	4	US-09-035-648-17	Sequence 17, Appl
c 867	26.4	3.4	376	4	US-09-513-999C-946	Sequence 946, App	940	26.4	3.4	4972	3	US-09-001-951-17	Sequence 17, Appl
868	26.4	3.4	381	3	US-09-134-001C-1762	Sequence 1762, Ap	c 941	26.4	3.4	4972	4	US-08-818-829-17	Sequence 17, Appl
869	26.4	3.4	388	3	US-08-746-160-4	Sequence 4, Appli	c 942	26.4	3.4	5053	4	US-08-961-527-187	Sequence 187, App
870	26.4	3.4	388	3	US-08-810-324-3	Sequence 3, Appli	943	26.4	3.4	5219	4	US-10-204-708-51	Sequence 51, Appl
871	26.4	3.4	389	2	US-08-808-277A-4	Sequence 4, Appli	944	26.4	3.4	6669	4	US-10-204-708-6	Sequence 6, Appli
872	26.4	3.4	389	2	US-08-808-277A-38	Sequence 6, Appli	945	26.4	3.4	8334	4	US-09-543-681A-1952	Sequence 1952, Ap
873	26.4	3.4	390	4	US-09-311-784A-38	Sequence 38, Appl	c 946	26.4	3.4	9726	4	US-09-841-786-8	Sequence 8, Appli
874	26.4	3.4	396	4	US-09-248-796A-1222	Sequence 1222, Ap	c 947	26.4	3.4	11130	4	US-09-841-786-15	Sequence 15, Appl
875	26.4	3.4	402	1	US-08-405-034-3	Sequence 3, Appli	948	26.4	3.4	13205	4	US-09-835-811-3	Sequence 3, Appli
c 876	26.4	3.4	415	4	US-09-513-999C-16647	Sequence 16647, A	949	26.4	3.4	16550	4	US-08-916-421B-3	Sequence 3, Appli
c 877	26.4	3.4	420	4	US-09-671-317-114	Sequence 114, App	950	26.4	3.4	16550	4	US-09-692-570-3	Sequence 3, Appli
c 878	26.4	3.4	422	4	US-09-270-767-13938	Sequence 13938, A	951	26.4	3.4	31063	4	US-09-596-002-20	Sequence 20, Appl
879	26.4	3.4	450	3	US-08-862-124-4	Sequence 4, Appli	c 952	26.4	3.4	51719	4	US-09-918-686-2	Sequence 2, Appli
c 880	26.4	3.4	450	3	US-08-862-124-6	Sequence 6, Appli	953	26.4	3.4	53526	3	US-08-658-136-2	Sequence 2, Appli
c 881	26.4	3.4	501	4	US-09-107-532A-1294	Sequence 1294, Ap	954	26.4	3.4	53577	3	US-08-658-136-1	Sequence 1, Appli
882	26.4	3.4	535	4	US-08-956-171E-1028	Sequence 1028, Ap	955	26.4	3.4	54550	4	US-10-327-189-42	Sequence 42, Appl
883	26.4	3.4	535	4	US-08-781-986A-1028	Sequence 1028, Ap	956	26.4	3.4	56516	2	US-08-996-306-1	Sequence 1, Appli
c 884	26.4	3.4	543	4	US-09-134-000C-344	Sequence 344, App	957	26.4	3.4	56516	3	US-09-338-907-1	Sequence 1, Appli
c 885	26.4	3.4	555	4	US-09-270-767-998	Sequence 998, App	958	26.4	3.4	56516	3	US-09-218-207-1	Sequence 1, Appli
c 886	26.4	3.4	555	4	US-09-270-767-16280	Sequence 16280, A	959	26.4	3.4	56520	3	US-09-338-907-179	Sequence 179, App
c 887	26.4	3.4	573	4	US-09-134-000C-2670	Sequence 2670, Ap	960	26.4	3.4	56520	3	US-09-218-207-179	Sequence 179, App
c 888	26.4	3.4	597	4	US-09-543-681A-1563	Sequence 1563, Ap	961	26.4	3.4	70000	4	US-09-851-896-3	Sequence 3, Appli
c 889	26.4	3.4	612	4	US-09-513-999C-83	Sequence 83, Appl	c 962	26.4	3.4	81001	4	US-09-750-580-1	Sequence 1, Appli
c 890	26.4	3.4	632	4	US-09-620-312D-486	Sequence 486, App	c 963	26.4	3.4	92139	4	US-09-918-686-1	Sequence 1, Appli
891	26.4	3.4	708	4	US-09-472-087-40	Sequence 40, Appl	c 964	26.4	3.4	99916	4	US-09-816-095-3	Sequence 3, Appli
892	26.4	3.4	708	4	US-09-472-087-56	Sequence 56, Appl	965	26.4	3.4	152331	3	US-09-128-155-16	Sequence 16, Appl
c 893	26.4	3.4	777	4	US-09-543-681A-441	Sequence 441, App	c 966	26.4	3.4	176373	3	US-09-128-155-17	Sequence 17, Appl
c 894	26.4	3.4	819	4	US-09-107-532A-3284	Sequence 3284, Ap	967	26.2	3.4	179	4	US-09-621-976-15323	Sequence 15323, A
895	26.4	3.4	861	4	US-09-134-000C-267	Sequence 267, App	968	26.2	3.4	221	4	US-09-513-999C-14455	Sequence 14455, A
896	26.4	3.4	876	4	US-09-583-110-1540	Sequence 1540, Ap	969	26.2	3.4	273	4	US-09-513-999C-25314	Sequence 25314, A
c 897	26.4	3.4	909	4	US-09-107-532A-3270	Sequence 3270, Ap	c 970	26.2	3.4	288	1	US-08-225-473-4	Sequence 4, Appli
898	26.4	3.4	930	4	US-09-540-236-1102	Sequence 1102, Ap	c 971	26.2	3.4	309	4	US-09-513-999C-3507	Sequence 3507, Ap
899	26.4	3.4	1056	4	US-09-248-796A-9572	Sequence 9572, Ap	972	26.2	3.4	375	4	US-09-270-767-9438	Sequence 9438, Ap
900	26.4	3.4	1122	4	US-09-328-352-640	Sequence 640, App	973	26.2	3.4	375	4	US-09-270-767-24720	Sequence 24720, A
c 901	26.4	3.4	1167	4	US-09-134-000C-2473	Sequence 2473, Ap	974	26.2	3.4	398	4	US-09-513-999C-13068	Sequence 13068, A
c 902	26.4	3.4	1219	4	US-09-270-767-30616	Sequence 30616, A	c 975	26.2	3.4	432	4	US-09-513-999C-20111	Sequence 20111, A
c 903	26.4	3.4	1233	4	US-09-856-486-13	Sequence 13, Appl	c 976	26.2	3.4	504	4	US-09-270-767-6141	Sequence 6141, Ap

c 977	26.2	3.4	504	4	US-09-270-767-21423	Sequence 21423, A	1050	26.2	3.4	14255	1	US-08-327-392-1	Sequence 1, Appli
c 978	26.2	3.4	511	4	US-09-513-999C-10722	Sequence 10722, A	1051	26.2	3.4	14255	1	US-08-306-691B-55	Sequence 55, Appl
979	26.2	3.4	528	4	US-09-328-352-3188	Sequence 3188, Ap	1052	26.2	3.4	14255	3	US-08-545-860D-1	Sequence 1, Appli
980	26.2	3.4	564	4	US-09-621-976-225	Sequence 225, App	1053	26.2	3.4	14255	5	PCT-US94-04496-1	Sequence 1, Appli
c 981	26.2	3.4	720	4	US-09-248-796A-13544	Sequence 13544, A	c1054	26.2	3.4	31728	3	US-09-453-702B-64	Sequence 64, Appl
982	26.2	3.4	785	4	US-09-270-767-28382	Sequence 28382, A	c1055	26.2	3.4	33140	4	US-09-596-002-23	Sequence 23, Appl
983	26.2	3.4	816	4	US-09-270-767-4369	Sequence 4369, Ap	1056	26.2	3.4	41684	4	US-09-536-059-1	Sequence 1, Appli
984	26.2	3.4	816	4	US-09-270-767-19651	Sequence 19651, A	1057	26.2	3.4	42235	3	US-09-199-637A-1	Sequence 1, Appli
c 985	26.2	3.4	825	4	US-09-248-796A-10866	Sequence 10866, A	c1058	26.2	3.4	161652	4	US-09-497-855A-40	Sequence 40, Appl
c 986	26.2	3.4	903	4	US-09-248-796A-4747	Sequence 4747, Ap	1059	26.2	3.4	168174	4	US-10-071-411A-63	Sequence 63, Appl
c 987	26.2	3.4	942	4	US-09-248-796A-4596	Sequence 4596, Ap	1060	26.2	3.4	168273	4	US-10-071-411A-2	Sequence 2, Appli
c 988	26.2	3.4	1019	1	US-08-225-473-2	Sequence 2, Appli	1061	26	3.4	225	4	US-09-248-796A-8831	Sequence 8831, Ap
989	26.2	3.4	1082	4	US-09-072-596-299	Sequence 299, App	c1062	26	3.4	251	4	US-09-313-294A-1804	Sequence 1804, Ap
990	26.2	3.4	1082	4	US-09-072-596-304	Sequence 304, App	1063	26	3.4	314	4	US-09-513-999C-24049	Sequence 24049, A
c 991	26.2	3.4	1143	4	US-09-248-796A-2316	Sequence 2316, Ap	1064	26	3.4	344	4	US-09-513-999C-27929	Sequence 27929, A
c 992	26.2	3.4	1227	4	US-09-125-619-1	Sequence 1, Appli	1065	26	3.4	345	2	US-08-263-911-3	Sequence 3, Appli
c 993	26.2	3.4	1227	4	US-10-222-566-1	Sequence 1, Appli	c1066	26	3.4	363	4	US-09-248-796A-13221	Sequence 13221, A
c 994	26.2	3.4	1227	4	US-10-143-024A-1	Sequence 1, Appli	c1067	26	3.4	426	4	US-09-710-279-1717	Sequence 1717, Ap
c 995	26.2	3.4	1287	3	US-09-134-001C-2366	Sequence 2366, Ap	1068	26	3.4	445	4	US-09-270-767-7307	Sequence 7307, Ap
996	26.2	3.4	1325	4	US-08-482-934A-9	Sequence 9, Appli	1069	26	3.4	445	4	US-09-270-767-22589	Sequence 22589, A
c 997	26.2	3.4	1368	4	US-09-248-796A-11323	Sequence 11323, A	c1070	26	3.4	467	4	US-09-649-747A-6	Sequence 6, Appli
c 998	26.2	3.4	1383	4	US-09-543-681A-4023	Sequence 4023, Ap	1071	26	3.4	477	4	US-09-248-796A-13407	Sequence 13407, A
999	26.2	3.4	1440	4	US-09-248-796A-1180	Sequence 5920, Ap	c1072	26	3.4	484	4	US-09-621-976-848	Sequence 848, App
1000	26.2	3.4	1669	4	US-09-149-476-133	Sequence 133, App	c1073	26	3.4	493	4	US-09-513-999C-3919	Sequence 3919, Ap
1001	26.2	3.4	1725	4	US-09-248-796A-1180	Sequence 1180, Ap	c1074	26	3.4	504	4	US-09-248-796A-5596	Sequence 5596, Ap
1002	26.2	3.4	1785	4	US-09-117-415B-1	Sequence 1, Appli	c1075	26	3.4	534	4	US-09-583-110-1031	Sequence 1031, Ap
1003	26.2	3.4	1820	2	US-08-757-046A-4	Sequence 4, Appli	1076	26	3.4	571	3	US-08-858-207A-262	Sequence 262, App
1004	26.2	3.4	1820	3	US-09-447-208-4	Sequence 4, Appli	c1077	26	3.4	604	4	US-09-288-143-62	Sequence 62, Appl
1005	26.2	3.4	1820	3	US-09-135-988-4	Sequence 4, Appli	c1078	26	3.4	605	4	US-09-621-976-945	Sequence 945, App
1006	26.2	3.4	1820	3	US-09-277-716-4	Sequence 4, Appli	1079	26	3.4	621	4	US-09-270-767-8444	Sequence 8444, Ap
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1008	26.2	3.4	1820	4	US-08-908-909-4	Sequence 4, Appli	1081	26	3.4	723	4	US-09-248-796A-13224	Sequence 13224, A
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1010	26.2	3.4	1820	4	US-08-990-103-4	Sequence 4, Appli	1083	26	3.4	725	2	US-08-392-338A-20	Sequence 20, Appl
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1012	26.2	3.4	1820	4	US-10-126-139-4	Sequence 4, Appli	1085	26	3.4	725	3	US-09-166-750-20	Sequence 20, Appl
1013	26.2	3.4	1820	4	US-10-126-798-4	Sequence 4, Appli	1086	26	3.4	725	3	US-09-166-093-20	Sequence 20, Appl
1014	26.2	3.4	1820	4	US-10-126-777-4	Sequence 4, Appli	1087	26	3.4	725	3	US-09-172-019-20	Sequence 20, Appl
1015	26.2	3.4	1842	4	US-09-117-415B-21	Sequence 21, Appl	1088	26	3.4	725	3	US-09-166-094-10	Sequence 10, Appl
1016	26.2	3.4	1896	4	US-09-117-415B-17	Sequence 17, Appl	1089	26	3.4	725	4	US-09-443-213-20	Sequence 20, Appl
1017	26.2	3.4	1896	4	US-09-117-415B-19	Sequence 19, Appl	1090	26	3.4	725	5	PCT-US93-11138-11	Sequence 11, Appl
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1021	26.2	3.4	2277	3	US-09-347-878-53	Sequence 53, Appl	1094	26	3.4	731	3	US-09-172-019-10	Sequence 10, Appl
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1125	26	3.4	856	3	US-08-463-903-16	Sequence 16, Appl	1198	26	3.4	2165	2	US-08-263-911-8	Sequence 8, Appli
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1167	26	3.4	1361	3	US-07-935-695-21	Sequence 21, Appl	1240	26	3.4	5966	4	US-08-956-171E-22	Sequence 22, Appl
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1175	26	3.4	1460	4	US-09-443-213-18	Sequence 18, Appl	c1248	26	3.4	13149	3	US-09-004-838-87	Sequence 87, Appl
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1189	26	3.4	1908	4	US-09-569-098A-50	Sequence 50, Appl	c1262	26	3.4	193303	4	US-09-497-855A-44	Sequence 44, Appl
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1194	26	3.4	1991	4	US-09-569-098A-4	Sequence 4, Appli	1267	25.8	3.4	305	4	US-09-401-064-294	Sequence 294, App
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c1270	25.8	3.4	406	4	US-09-370-838-235	Sequence 235, App	c1343	25.8	3.4	1398	4	US-09-658-824-322	Sequence 322, App
c1271	25.8	3.4	406	4	US-09-854-133-235	Sequence 235, App	c1344	25.8	3.4	1422	4	US-09-248-796A-4567	Sequence 4567, Ap
c1272	25.8	3.4	418	4	US-09-270-767-1657	Sequence 1657, Ap	c1345	25.8	3.4	1443	4	US-09-107-532A-2506	Sequence 2506, Ap
c1273	25.8	3.4	418	4	US-09-270-767-16939	Sequence 16939, A	c1346	25.8	3.4	1452	4	US-09-134-000C-391	Sequence 391, App
c1274	25.8	3.4	464	4	US-09-270-767-8057	Sequence 8057, Ap	c1347	25.8	3.4	1455	4	US-09-489-039A-3883	Sequence 3883, Ap
c1275	25.8	3.4	464	4	US-09-270-767-23339	Sequence 23339, A	c1348	25.8	3.4	1547	4	US-09-270-767-11728	Sequence 11728, A
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1279	25.8	3.4	515	1	US-08-550-544-5	Sequence 5, Appli	c1352	25.8	3.4	1827	2	US-08-824-878-2	Sequence 2, Appli
c1280	25.8	3.4	516	4	US-10-101-464A-295	Sequence 295, App	c1353	25.8	3.4	1827	3	US-09-353-688-2	Sequence 2, Appli
1281	25.8	3.4	544	4	US-09-621-976-1811	Sequence 1811, Ap	c1354	25.8	3.4	1827	4	US-09-248-796A-6075	Sequence 6075, Ap
c1282	25.8	3.4	546	4	US-09-248-796A-1778	Sequence 1778, Ap	c1355	25.8	3.4	1863	2	US-08-455-073A-3	Sequence 3, Appli
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c1284	25.8	3.4	564	4	US-09-248-796A-5115	Sequence 5115, Ap	c1357	25.8	3.4	1978	4	US-09-639-609-1	Sequence 90, Appl
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c1287	25.8	3.4	573	1	US-08-319-590-24	Sequence 24, Appl	c1360	25.8	3.4	2382	4	US-09-640-173-180	Sequence 180, App
c1288	25.8	3.4	573	1	US-08-487-001A-24	Sequence 24, Appl	c1361	25.8	3.4	2382	4	US-09-713-550-180	Sequence 180, App
c1289	25.8	3.4	573	2	US-08-630-822A-24	Sequence 24, Appl	c1362	25.8	3.4	2382	4	US-09-825-294-180	Sequence 180, App
c1290	25.8	3.4	573	2	US-08-711-905-24	Sequence 24, Appl	c1363	25.8	3.4	2382	4	US-09-970-966-180	Sequence 180, App
c1291	25.8	3.4	573	2	US-09-005-069-24	Sequence 24, Appl	c1364	25.8	3.4	2395	3	US-09-724-864-24	Sequence 24, Appl
1292	25.8	3.4	588	4	US-09-107-532A-244	Sequence 244, App	c1365	25.8	3.4	2463	4	US-09-328-352-1640	Sequence 24, Appl
c1293	25.8	3.4	591	1	US-08-487-001A-34	Sequence 34, Appl	c1366	25.8	3.4	2678	3	US-09-232-160-5	Sequence 5, Appli
c1294	25.8	3.4	591	2	US-08-630-822A-34	Sequence 34, Appl	c1367	25.8	3.4	2816	4	US-09-793-451-774	Sequence 774, App
c1295	25.8	3.4	591	2	US-09-005-069-34	Sequence 34, Appl	c1368	25.8	3.4	3015	4	US-09-248-796A-4016	Sequence 4016, Ap
c1296	25.8	3.4	591	4	US-09-710-279-777	Sequence 777, App	c1369	25.8	3.4	3069	4	US-09-514-907A-5	Sequence 5, Appli
1297	25.8	3.4	594	4	US-09-710-279-1883	Sequence 1883, Ap	c1370	25.8	3.4	3069	4	US-09-896-994-5	Sequence 5, Appli
c1298	25.8	3.4	605	3	US-09-385-982-501	Sequence 501, App	c1371	25.8	3.4	3119	4	US-09-710-279-4270	Sequence 4270, Ap
c1299	25.8	3.4	618	4	US-09-270-767-8516	Sequence 8516, Ap	c1372	25.8	3.4	3263	3	US-08-714-918-20	Sequence 20, Appl
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1301	25.8	3.4	654	4	US-08-956-171B-1180	Sequence 1180, Ap	c1374	25.8	3.4	3263	3	US-09-265-315-20	Sequence 20, Appl
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1304	25.8	3.4	697	3	US-08-998-416-912	Sequence 912, App	c1377	25.8	3.4	3263	4	US-09-527-745-20	Sequence 20, Appl
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1307	25.8	3.4	726	3	US-09-134-001C-2656	Sequence 2656, Ap	c1380	25.8	3.4	3443	4	US-09-886-683A-3	Sequence 3, Appli
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c1309	25.8	3.4	801	4	US-09-252-991A-1475	Sequence 1475, Ap	c1382	25.8	3.4	3452	4	US-09-976-594-856	Sequence 856, App
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1312	25.8	3.4	833	4	US-09-270-767-30471	Sequence 30471, A	c1385	25.8	3.4	3519	4	US-09-710-279-3836	Sequence 3836, Ap
c1313	25.8	3.4	867	4	US-09-107-532A-407	Sequence 407, App	c1386	25.8	3.4	3592	3	US-08-714-918-63	Sequence 63, Appl
1314	25.8	3.4	882	4	US-09-583-110-351	Sequence 351, App	c1387	25.8	3.4	3592	3	US-09-265-315-63	Sequence 63, Appl
c1315	25.8	3.4	915	4	US-09-328-352-3163	Sequence 3163, Ap	c1388	25.8	3.4	3592	3	US-09-265-315-63	Sequence 63, Appl
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c1317	25.8	3.4	954	3	US-08-462-625-37	Sequence 37, Appl	c1390	25.8	3.4	3592	4	US-09-528-709-63	Sequence 63, Appl
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c1329	25.8	3.4	1098	4	US-09-248-796A-412	Sequence 412, App	c1402	25.8	3.4	5852	1	US-07-867-106-2	Sequence 2, Appli
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1331	25.8	3.4	1244	4	US-09-265-540E-3	Sequence 3, Appli	c1404	25.8	3.4	10467	4	US-10-204-708-2	Sequence 2, Appli
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1334	25.8	3.4	1315	4	US-09-710-279-4437	Sequence 4437, Ap	c1407	25.8	3.4	11464	3	US-08-884-324-13	Sequence 13, Appl
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RESULT 4

US-09-583-110-486/c

; Sequence 486, Application US/09583110

; Patent No. 6699703

; GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al.

; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus

; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics

; FILE REFERENCE: PATH00-07A

; CURRENT APPLICATION NUMBER: US/09/583,110

; CURRENT FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: US 09/107,433

; PRIOR FILING DATE: 1998-06-30

; PRIOR APPLICATION NUMBER: US 60/085,131

; PRIOR FILING DATE: 1998-05-12

; PRIOR APPLICATION NUMBER: US 60/051,553

; PRIOR FILING DATE: 1997-07-02

; NUMBER OF SEQ ID NOS: 5322

; SEQ ID NO 486

; LENGTH: 393

; TYPE: DNA

; ORGANISM: Streptococcus pneumoniae

US-09-583-110-486

Query Match 4.7%; Score 35.8; DB 4; Length 393;

Best Local Similarity 48.3%; Pred. No. 0.24;

Matches 100; Conservative 0; Mismatches 107; Indels 0; Gaps 0;

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Qy 462 GTGGTTTTCATGACTCTTGTCACCTCCTACTGTTTCAATAAACCCACCAGTAACGA 521

Db 151 TTTCTTTAGTCAAATAACCTGTTCTCTATAACTGGTAGTAATAACAAAATTACTAAAAG 92

Qy 522 CACCATGGCGAGTGGCTGGAGAGCATCTAGTTTCCACTTCGATTTCTGAAGAAAAACAACA 581

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Qy 582 TAGGCTTATCCACTTCTCAGTATTTT 608

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RESULT 5

US-09-621-976-2813

; Sequence 2813, Application US/09621976

; Patent No. 6639063

; GENERAL INFORMATION:

; APPLICANT: Dumas Milne Edwards, J.B.

; APPLICANT: Jobert, S.

; APPLICANT: Giordano, J.Y.

; TITLE OF INVENTION: ESTs and Encoded Human Proteins.

; FILE REFERENCE: GENSET.054PR2

; CURRENT APPLICATION NUMBER: US/09/621,976

; CURRENT FILING DATE: 2000-07-21

; NUMBER OF SEQ ID NOS: 19335

; SOFTWARE: Patent.pm

; SEQ ID NO 2813

; LENGTH: 832

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 235..399

US-09-621-976-2813

Query Match 4.7%; Score 35.8; DB 4; Length 832;

Best Local Similarity 9.6%; Pred. No. 0.35;

Matches 16; Conservative 92; Mismatches 59; Indels 0; Gaps 0;

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Qy 641 TGTTTGGGCTCAGTCAGATAGTCATCGGTTTCCTTGGCTGTCTGTGTGGAGTCTCTAAGC 700

Db 79 KKKKKKGYMMWYWGWRRSYMMAMWTRWTGYAYRSMYWRRCWKKKAYRKTTTCYSS 138

Qy 701 GAAGAAGTCAAATTTGTGTAGTTTAAATGGGAATAAAATGTAAGTATCA 747

Db 139 KGWTWKRWKKAATTTWKKTYWAAATRYMMWMMCWTKRWRASWYCW 185

RESULT 6

US-09-589-733C-5/c

; Sequence 5, Application US/09589733C

; Patent No. 6677503

; GENERAL INFORMATION:

; APPLICANT: Bidney, Dennis L.

; APPLICANT: Crasta, Oswald R.

; APPLICANT: Duvick, Jon

; APPLICANT: Hu, Xu

; APPLICANT: Lu, Guihua

; TITLE OF INVENTION: Sunflower Anti-Pathogenic Proteins and

; TITLE OF INVENTION: Genes and their Uses

; FILE REFERENCE: 5718-90

; CURRENT APPLICATION NUMBER: US/09/589,733C

; CURRENT FILING DATE: 2000-06-08

; PRIOR APPLICATION NUMBER: 60/140,646

; PRIOR FILING DATE: 1999-06-23

; PRIOR APPLICATION NUMBER: 60/162,904

; PRIOR FILING DATE: 1999-11-01

; NUMBER OF SEQ ID NOS: 41

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 5

; LENGTH: 1809

; TYPE: DNA

; ORGANISM: Helianthus annuus

US-09-589-733C-5

Query Match 4.5%; Score 34.8; DB 4; Length 1809;

Best Local Similarity 50.6%; Pred. No. 1.1;

Matches 84; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

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Qy 319 GGTGCTCTGTATTGCTGATGATATCCATCCAGGCTCTCTTAAAGGTCCTCTCATGTGT 378

Db 928 CGTACGGTTTCTGAGTGGTGTTCCTATATATACTCGGTGTTAAGCTGAACCTCTGATGAGT 869

Qy 379 AATTCTCCAAGCAACAGTAATGCCAATGTGAATTTTCATTTGAAAA 424

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RESULT 7

US-09-751-389-3/c

; Sequence 3, Application US/09751389

; Patent No. 6630334

; GENERAL INFORMATION:

; APPLICANT: GUEGLER, Karl et al

; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: CL001067

; CURRENT APPLICATION NUMBER: US/09/751,389

; CURRENT FILING DATE: 2001-01-02

; NUMBER OF SEQ ID NOS: 8

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and is derived by analysis of the total score distribution.

SUMMARIES

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624	766	100.0	766	15	US-10-063-742-47	Sequence 47, Appl
716	766	100.0	766	15	US-10-063-550-47	Sequence 47, Appl
740	748.6	97.7	2294	13	US-10-087-192-65	Sequence 65, Appl
741	748.6	97.7	2294	18	US-10-331-053-35	Sequence 35, Appl
742	747	97.5	2308	17	US-10-755-889-507	Sequence 507, App
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744	475.2	62.0	1504	18	US-10-331-053-32	Sequence 32, Appl
745	332	43.3	37262	13	US-10-087-192-64	Sequence 64, Appl
746	332	43.3	37262	18	US-10-331-053-34	Sequence 34, Appl
747	264.2	34.5	351	10	US-09-803-719-950	Sequence 950, App
c 748	264	34.5	585	16	US-10-240-425-578	Sequence 578, App

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c 759	39.4	5.1	8034	16	US-10-342-887-1278	Sequence 1278, Ap
c 760	39	5.1	447	9	US-09-764-869-122	Sequence 122, App
c 761	39	5.1	447	14	US-10-091-504-122	Sequence 122, App
c 762	39	5.1	447	16	US-10-227-577-122	Sequence 122, App
c 763	38.8	5.1	3673778	15	US-10-312-841-2	Sequence 2, Appli
c 764	38.2	5.0	2579	18	US-10-425-115-24879	Sequence 24879, A
c 765	37.6	4.9	363	10	US-09-960-706-194	Sequence 194, App
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c 768	37	4.8	108182	13	US-10-087-192-1618	Sequence 1618, Ap
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784	35	4.6	759	15	US-10-027-632-15157	Sequence 15157, A
785	35	4.6	759	15	US-10-027-632-15158	Sequence 15158, A
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c 797	34.2	4.5	786431	15	US-10-412-277-3	Sequence 3, Appli
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c 807	33.8	4.4	4530	17	US-10-437-963-26968	Sequence 26968, A
c 808	33.8	4.4	290547	17	US-10-367-094-77	Sequence 77, Appl
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1006	31.2	4.1	3262	14	US-10-175-523-147	Sequence 147, App	1079	31	4.0	1701	15	US-10-027-632-264344	Sequence 264344,
1007	31.2	4.1	4800	10	US-09-764-891-8780	Sequence 8780, Ap	1080	31	4.0	1701	15	US-10-027-632-264345	Sequence 264345,
1008	31.2	4.1	4845	10	US-09-764-891-8781	Sequence 8781, Ap	1081	31	4.0	1701	15	US-10-027-632-264346	Sequence 264346,
1009	31.2	4.1	6450	13	US-10-096-710-2	Sequence 2, Appli	1082	31	4.0	1701	15	US-10-027-632-264347	Sequence 264347,
1010	31.2	4.1	6450	13	US-10-081-563-1	Sequence 1, Appli	1083	31	4.0	1701	15	US-10-027-632-264348	Sequence 264348,
1011	31.2	4.1	6450	14	US-10-052-092-1	Sequence 1, Appli	1084	31	4.0	1701	15	US-10-027-632-264345	Sequence 264345,
1012	31.2	4.1	6450	14	US-10-052-092-7	Sequence 7, Appli	c1085	31	4.0	2561	16	US-10-424-599-66239	Sequence 66239, A
1013	31.2	4.1	6450	15	US-10-207-655-60	Sequence 60, Appl	c1086	31	4.0	3051	17	US-10-473-115-3	Sequence 3, Appli
1014	31.2	4.1	6450	15	US-10-177-293-127	Sequence 127, App	c1087	31	4.0	3316	15	US-10-242-056-58	Sequence 58, Appl
1015	31.2	4.1	6450	15	US-10-027-983-3	Sequence 3, Appli	c1088	31	4.0	4396	17	US-10-437-963-45548	Sequence 45548, A
1016	31.2	4.1	6450	15	US-10-007-926A-422	Sequence 422, App	c1089	31	4.0	35680	13	US-10-087-192-1186	Sequence 1186, Ap
1017	31.2	4.1	6450	15	US-10-437-107-1	Sequence 1, Appli	c1090	31	4.0	37278	17	US-10-322-281-21	Sequence 21, Appl
1018	31.2	4.1	6450	15	US-10-437-107-7	Sequence 7, Appli	1091	31	4.0	101782	17	US-10-741-601-5661	Sequence 5661, Ap
1019	31.2	4.1	6450	15	US-10-392-274-1	Sequence 1, Appli	1092	31	4.0	180216	9	US-09-835-232-6	Sequence 6, Appli
1020	31.2	4.1	6450	15	US-10-448-753-3	Sequence 3, Appli	1093	31	4.0	180216	15	US-10-308-485-6	Sequence 6, Appli
1021	31.2	4.1	6450	15	US-10-172-118-435	Sequence 435, App	1094	31	4.0	185458	18	US-10-719-993-6864	Sequence 6864, Ap
1022	31.2	4.1	6450	15	US-10-388-360-303	Sequence 303, App	1095	31	4.0	246940	17	US-10-322-696-58	Sequence 58, Appl
1023	31.2	4.1	6450	16	US-10-342-887-435	Sequence 435, App	1096	31	4.0	2731748	17	US-10-297-465A-1	Sequence 1, Appli
1024	31.2	4.1	6450	18	US-10-370-715B-75	Sequence 75, Appl	c1097	31	4.0	3673778	15	US-10-312-841-2	Sequence 2, Appli
1025	31.2	4.1	6450	18	US-10-896-419-1	Sequence 1, Appli	1098	30.8	4.0	265	18	US-10-357-930-15233	Sequence 15233, A
1026	31.2	4.1	6450	18	US-10-896-419-7	Sequence 7, Appli	1099	30.8	4.0	285	18	US-10-357-930-6064	Sequence 6064, Ap
1027	31.2	4.1	6608	14	US-10-198-846-11305	Sequence 11305, A	1100	30.8	4.0	303	18	US-10-357-930-2492	Sequence 2492, Ap
1028	31.2	4.1	8566	15	US-10-027-983-10	Sequence 10, Appl	1101	30.8	4.0	323	18	US-10-357-930-6041	Sequence 6041, Ap
1029	31.2	4.1	8566	15	US-10-448-753-10	Sequence 10, Appl	1102	30.8	4.0	327	18	US-10-357-930-216	Sequence 216, App
1030	31.2	4.1	22073	10	US-09-764-891-7351	Sequence 7351, Ap	1103	30.8	4.0	328	18	US-10-357-930-453	Sequence 453, App
1031	31.2	4.1	30304	17	US-10-367-094-128	Sequence 128, App	1104	30.8	4.0	331	18	US-10-357-930-11336	Sequence 11336, A
1032	31.2	4.1	54810	18	US-10-417-375-91	Sequence 91, Appl	1105	30.8	4.0	341	18	US-10-357-930-15210	Sequence 15210, A
c1033	31.2	4.1	105664	14	US-10-175-523-97	Sequence 97, Appl	1106	30.8	4.0	344	18	US-10-357-930-7314	Sequence 7314, Ap
c1034	31.2	4.1	247682	16	US-10-235-192A-28	Sequence 28, Appl	1107	30.8	4.0	346	18	US-10-357-930-9622	Sequence 9622, Ap
1035	31.2	4.1	326014	9	US-09-731-231A-3	Sequence 3, Appli	1108	30.8	4.0	346	18	US-10-357-930-15206	Sequence 15206, A
1036	31.2	4.1	326014	17	US-10-751-985-3	Sequence 3, Appli	1109	30.8	4.0	355	18	US-10-357-930-2904	Sequence 2904, Ap
1037	31.2	4.1	392000	15	US-10-027-983-11	Sequence 11, Appl	1110	30.8	4.0	356	18	US-10-357-930-12073	Sequence 12073, A
1038	31.2	4.1	392000	15	US-10-448-753-11	Sequence 11, Appl	1111	30.8	4.0	361	18	US-10-357-930-10249	Sequence 10249, A
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1040	31.2	4.1	653122	13	US-10-087-192-226	Sequence 226, App	1113	30.8	4.0	363	18	US-10-357-930-6777	Sequence 6777, Ap

1114	30.8	4.0	366	18	US-10-357-930-9011	Sequence 9011, Ap	1187	30.8	4.0	429	18	US-10-357-930-3104	Sequence 3104, Ap
1115	30.8	4.0	372	18	US-10-357-930-11525	Sequence 11525, A	1188	30.8	4.0	430	18	US-10-357-930-12134	Sequence 12134, A
1116	30.8	4.0	374	18	US-10-357-930-11771	Sequence 11771, A	1189	30.8	4.0	432	18	US-10-357-930-12184	Sequence 12184, A
1117	30.8	4.0	374	18	US-10-357-930-11795	Sequence 11795, A	1190	30.8	4.0	432	18	US-10-357-930-33066	Sequence 33066, A
1118	30.8	4.0	374	18	US-10-357-930-12156	Sequence 12156, A	1191	30.8	4.0	434	18	US-10-357-930-31710	Sequence 31710, A
1119	30.8	4.0	376	18	US-10-357-930-10414	Sequence 10414, A	1192	30.8	4.0	434	18	US-10-357-930-32984	Sequence 32984, A
1120	30.8	4.0	380	18	US-10-357-930-2626	Sequence 2626, Ap	1193	30.8	4.0	435	18	US-10-357-930-3015	Sequence 3015, Ap
c1121	30.8	4.0	381	18	US-10-425-115-44413	Sequence 44413, A	1194	30.8	4.0	435	18	US-10-357-930-32875	Sequence 32875, A
1122	30.8	4.0	381	18	US-10-357-930-2723	Sequence 2723, Ap	1195	30.8	4.0	435	18	US-10-357-930-33146	Sequence 33146, A
1123	30.8	4.0	381	18	US-10-357-930-10163	Sequence 10163, A	1196	30.8	4.0	435	18	US-10-357-930-42072	Sequence 42072, A
1124	30.8	4.0	383	18	US-10-357-930-11698	Sequence 11698, A	1197	30.8	4.0	438	18	US-10-357-930-7044	Sequence 7044, Ap
1125	30.8	4.0	383	18	US-10-357-930-32508	Sequence 32508, A	1198	30.8	4.0	439	18	US-10-357-930-36210	Sequence 36210, A
1126	30.8	4.0	383	18	US-10-357-930-36032	Sequence 36032, A	1199	30.8	4.0	439	18	US-10-357-930-45263	Sequence 45263, A
1127	30.8	4.0	385	18	US-10-357-930-11532	Sequence 11532, A	1200	30.8	4.0	440	18	US-10-357-930-33110	Sequence 33110, A
1128	30.8	4.0	385	18	US-10-357-930-32833	Sequence 32833, A	1201	30.8	4.0	440	18	US-10-357-930-41801	Sequence 41801, A
1129	30.8	4.0	388	18	US-10-357-930-10513	Sequence 10513, A	1202	30.8	4.0	440	18	US-10-357-930-42036	Sequence 42036, A
1130	30.8	4.0	390	16	US-10-424-599-91710	Sequence 91710, A	1203	30.8	4.0	441	18	US-10-357-930-2363	Sequence 2363, Ap
1131	30.8	4.0	390	18	US-10-357-930-2987	Sequence 2987, Ap	1204	30.8	4.0	441	18	US-10-357-930-37013	Sequence 37013, A
1132	30.8	4.0	391	18	US-10-357-930-2725	Sequence 2725, Ap	1205	30.8	4.0	441	18	US-10-357-930-41893	Sequence 41893, A
1133	30.8	4.0	391	18	US-10-357-930-11661	Sequence 11661, A	1206	30.8	4.0	442	18	US-10-357-930-36750	Sequence 36750, A
1134	30.8	4.0	391	18	US-10-357-930-11890	Sequence 11890, A	1207	30.8	4.0	443	18	US-10-357-930-32718	Sequence 32718, A
1135	30.8	4.0	392	18	US-10-357-930-31288	Sequence 31288, A	1208	30.8	4.0	443	18	US-10-357-930-41759	Sequence 41759, A
1136	30.8	4.0	393	18	US-10-357-930-11894	Sequence 11894, A	1209	30.8	4.0	443	18	US-10-357-930-41824	Sequence 41824, A
c1137	30.8	4.0	394	16	US-10-424-599-113745	Sequence 113745, A	1210	30.8	4.0	445	18	US-10-357-930-2769	Sequence 2769, Ap
1138	30.8	4.0	395	18	US-10-357-930-15391	Sequence 15391, A	1211	30.8	4.0	446	18	US-10-357-930-33189	Sequence 33189, A
1139	30.8	4.0	396	18	US-10-357-930-11812	Sequence 11812, A	1212	30.8	4.0	446	18	US-10-357-930-41865	Sequence 41865, A
1140	30.8	4.0	397	18	US-10-357-930-11938	Sequence 11938, A	1213	30.8	4.0	446	18	US-10-357-930-42114	Sequence 42114, A
1141	30.8	4.0	398	18	US-10-357-930-11546	Sequence 11546, A	1214	30.8	4.0	447	18	US-10-357-930-32988	Sequence 32988, A
1142	30.8	4.0	398	18	US-10-357-930-11892	Sequence 11892, A	1215	30.8	4.0	450	18	US-10-357-930-2647	Sequence 2647, Ap
1143	30.8	4.0	399	18	US-10-357-930-12017	Sequence 12017, A	1216	30.8	4.0	452	18	US-10-357-930-31426	Sequence 31426, A
1144	30.8	4.0	400	18	US-10-357-930-2805	Sequence 2805, Ap	1217	30.8	4.0	452	18	US-10-357-930-40396	Sequence 40396, A
1145	30.8	4.0	401	18	US-10-357-930-11703	Sequence 11703, A	1218	30.8	4.0	453	18	US-10-357-930-1059	Sequence 1059, Ap
1146	30.8	4.0	401	18	US-10-357-930-32697	Sequence 32697, A	c1219	30.8	4.0	459	16	US-10-424-599-51631	Sequence 51631, A
1147	30.8	4.0	402	18	US-10-357-930-2900	Sequence 2900, Ap	1220	30.8	4.0	462	18	US-10-357-930-33445	Sequence 33445, A
1148	30.8	4.0	402	18	US-10-357-930-11974	Sequence 11974, A	1221	30.8	4.0	462	18	US-10-357-930-33326	Sequence 33326, A
1149	30.8	4.0	402	18	US-10-357-930-31447	Sequence 31447, A	1222	30.8	4.0	464	18	US-10-357-930-33306	Sequence 33306, A
1150	30.8	4.0	402	18	US-10-357-930-43892	Sequence 43892, A	1223	30.8	4.0	464	18	US-10-357-930-40331	Sequence 40331, A
1151	30.8	4.0	406	18	US-10-357-930-2529	Sequence 2529, Ap	1224	30.8	4.0	464	18	US-10-357-930-40580	Sequence 40580, A
1152	30.8	4.0	406	18	US-10-357-930-11816	Sequence 11816, A	1225	30.8	4.0	464	18	US-10-357-930-40679	Sequence 40679, A
1153	30.8	4.0	407	18	US-10-357-930-2377	Sequence 2377, Ap	1226	30.8	4.0	464	18	US-10-357-930-42230	Sequence 42230, A
1154	30.8	4.0	407	18	US-10-357-930-33245	Sequence 33245, A	1227	30.8	4.0	464	18	US-10-357-930-45072	Sequence 45072, A
1155	30.8	4.0	407	18	US-10-357-930-42169	Sequence 42169, A	1228	30.8	4.0	468	18	US-10-357-930-33356	Sequence 33356, A
1156	30.8	4.0	410	18	US-10-357-930-10228	Sequence 10228, A	1229	30.8	4.0	468	18	US-10-357-930-40417	Sequence 40417, A
1157	30.8	4.0	410	18	US-10-357-930-12154	Sequence 12154, A	1230	30.8	4.0	469	18	US-10-357-930-33461	Sequence 33461, A
1158	30.8	4.0	411	18	US-10-357-930-6222	Sequence 6222, Ap	1231	30.8	4.0	469	18	US-10-357-930-42385	Sequence 42385, A
1159	30.8	4.0	411	18	US-10-357-930-36036	Sequence 36036, A	1232	30.8	4.0	469	18	US-10-357-930-45097	Sequence 45097, A
1160	30.8	4.0	414	18	US-10-357-930-32943	Sequence 32943, A	1233	30.8	4.0	484	13	US-10-027-632-194226	Sequence 194226, A
1161	30.8	4.0	414	18	US-10-357-930-41869	Sequence 41869, A	1234	30.8	4.0	484	15	US-10-027-632-194226	Sequence 194226, A
1162	30.8	4.0	416	18	US-10-357-930-2848	Sequence 2848, Ap	1235	30.8	4.0	496	18	US-10-357-930-6642	Sequence 6642, Ap
1163	30.8	4.0	416	18	US-10-357-930-32870	Sequence 32870, A	1236	30.8	4.0	504	18	US-10-357-930-60388	Sequence 60388, A
1164	30.8	4.0	417	18	US-10-357-930-2721	Sequence 2721, Ap	1237	30.8	4.0	517	18	US-10-357-930-39191	Sequence 39191, A
c1165	30.8	4.0	418	18	US-10-674-124A-1922	Sequence 1922, Ap	1238	30.8	4.0	520	18	US-10-357-930-36617	Sequence 36617, A
1166	30.8	4.0	418	18	US-10-357-930-33328	Sequence 33328, A	1239	30.8	4.0	520	18	US-10-357-930-41623	Sequence 41623, A
1167	30.8	4.0	418	18	US-10-357-930-32704	Sequence 32704, A	1240	30.8	4.0	541	18	US-10-357-930-6793	Sequence 6793, Ap
1168	30.8	4.0	419	18	US-10-357-930-994	Sequence 994, App	1241	30.8	4.0	560	13	US-10-027-632-41707	Sequence 41707, A
1169	30.8	4.0	419	18	US-10-357-930-31611	Sequence 31611, A	1242	30.8	4.0	560	15	US-10-027-632-41707	Sequence 41707, A
1170	30.8	4.0	419	18	US-10-357-930-32704	Sequence 32704, A	c1243	30.8	4.0	562	16	US-10-425-114-32414	Sequence 32414, A
1171	30.8	4.0	419	18	US-10-357-930-41796	Sequence 41796, A	1244	30.8	4.0	565	18	US-10-357-930-2697	Sequence 2697, Ap
1172	30.8	4.0	419	18	US-10-357-930-45093	Sequence 45093, A	1245	30.8	4.0	569	18	US-10-357-930-3120	Sequence 3120, Ap
1173	30.8	4.0	421	18	US-10-357-930-1245	Sequence 1245, Ap	1246	30.8	4.0	578	10	US-09-814-353-4867	Sequence 4867, Ap
1174	30.8	4.0	421	18	US-10-357-930-32967	Sequence 32967, A	1247	30.8	4.0	578	10	US-09-814-353-11164	Sequence 11164, A
1175	30.8	4.0	422	18	US-10-357-930-12273	Sequence 12273, A	c1248	30.8	4.0	584	13	US-10-027-632-41690	Sequence 41690, A
1176	30.8	4.0	422	18	US-10-357-930-31361	Sequence 31361, A	c1249	30.8	4.0	584	15	US-10-027-632-41691	Sequence 41691, A
1177	30.8	4.0	423	18	US-10-357-930-2643	Sequence 2643, Ap	c1250	30.8	4.0	584	15	US-10-027-632-41690	Sequence 41690, A
c1178	30.8	4.0	427	9	US-09-736-457-1152	Sequence 1152, Ap	c1251	30.8	4.0	584	15	US-10-027-632-41691	Sequence 41691, A
c1179	30.8	4.0	427	9	US-09-802-941-1152	Sequence 1152, Ap	c1252	30.8	4.0	591	13	US-10-027-632-70917	Sequence 70917, A
c1180	30.8	4.0	427	9	US-09-849-626-1152	Sequence 1152, Ap	c1253	30.8	4.0	591	13	US-10-027-632-70918	Sequence 70918, A
c1181	30.8	4.0	427	14	US-10-017-754-1152	Sequence 1152, Ap	c1254	30.8	4.0	591	13	US-10-027-632-294072	Sequence 294072, A
c1182	30.8	4.0	427	15	US-10-113-872-1152	Sequence 1152, Ap	c1255	30.8	4.0	591	13	US-10-027-632-294090	Sequence 294090, A
c1183	30.8	4.0	427	15	US-10-283-017-1152	Sequence 1152, Ap	c1256	30.8	4.0	591	15	US-10-027-632-70917	Sequence 70917, A
1184	30.8	4.0	428	18	US-10-357-930-33062	Sequence 33062, A	c1257	30.8	4.0	591	15	US-10-027-632-70918	Sequence 70918, A
1185	30.8	4.0	428	18	US-10-357-930-41988	Sequence 41988, A	c1258	30.8	4.0	591	15	US-10-027-632-294072	Sequence 294072, A
1186	30.8	4.0	429	18	US-10-357-930-2965	Sequence 2965, Ap	c1259	30.8	4.0	591	15	US-10-027-632-294090	Sequence 294090, A

1260	30.8	4.0	602	18	US-10-357-930-33064	Sequence 33064, A	c1333	30.6	4.0	450	13	US-10-027-632-72454	Sequence 72454, A
1261	30.8	4.0	602	18	US-10-357-930-36766	Sequence 36766, A	c1334	30.6	4.0	450	13	US-10-027-632-72455	Sequence 72455, A
1262	30.8	4.0	602	18	US-10-357-930-37278	Sequence 37278, A	c1335	30.6	4.0	450	13	US-10-027-632-72456	Sequence 72456, A
1263	30.8	4.0	602	18	US-10-357-930-39473	Sequence 39473, A	c1336	30.6	4.0	450	13	US-10-027-632-299106	Sequence 299106, A
1264	30.8	4.0	602	18	US-10-357-930-41438	Sequence 41438, A	c1337	30.6	4.0	450	13	US-10-027-632-299107	Sequence 299107, A
1265	30.8	4.0	602	18	US-10-357-930-41630	Sequence 41630, A	c1338	30.6	4.0	450	13	US-10-027-632-299108	Sequence 299108, A
1266	30.8	4.0	602	18	US-10-357-930-41644	Sequence 41644, A	c1339	30.6	4.0	450	13	US-10-027-632-312731	Sequence 312731, A
1267	30.8	4.0	602	18	US-10-357-930-41910	Sequence 41910, A	c1340	30.6	4.0	450	15	US-10-027-632-34324	Sequence 34324, A
1268	30.8	4.0	602	18	US-10-357-930-41914	Sequence 41914, A	c1341	30.6	4.0	450	15	US-10-027-632-34325	Sequence 34325, A
1269	30.8	4.0	602	18	US-10-357-930-41990	Sequence 41990, A	c1342	30.6	4.0	450	15	US-10-027-632-34326	Sequence 34326, A
1270	30.8	4.0	602	18	US-10-357-930-41992	Sequence 41992, A	c1343	30.6	4.0	450	15	US-10-027-632-34327	Sequence 34327, A
1271	30.8	4.0	602	18	US-10-357-930-42165	Sequence 42165, A	c1344	30.6	4.0	450	15	US-10-027-632-72453	Sequence 72453, A
1272	30.8	4.0	602	18	US-10-357-930-42250	Sequence 42250, A	c1345	30.6	4.0	450	15	US-10-027-632-72454	Sequence 72454, A
1273	30.8	4.0	602	18	US-10-357-930-42280	Sequence 42280, A	c1346	30.6	4.0	450	15	US-10-027-632-72455	Sequence 72455, A
1274	30.8	4.0	602	18	US-10-357-930-42369	Sequence 42369, A	c1347	30.6	4.0	450	15	US-10-027-632-72456	Sequence 72456, A
1275	30.8	4.0	602	18	US-10-357-930-43292	Sequence 43292, A	c1348	30.6	4.0	450	15	US-10-027-632-299106	Sequence 299106, A
1276	30.8	4.0	603	18	US-10-357-930-9039	Sequence 9039, Ap	c1349	30.6	4.0	450	15	US-10-027-632-299107	Sequence 299107, A
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c1459	30.4	4.0	1520	16	US-10-425-114-11429	Sequence 11429, A
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c1461	30.4	4.0	1794	16	US-10-424-599-21983	Sequence 21983, A
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1478	30.4	4.0	5421	15	US-10-311-455-105	Sequence 105, App
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1481	30.4	4.0	8131	15	US-10-311-455-869	Sequence 869, App
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1483	30.4	4.0	9087	16	US-10-221-613-140	Sequence 140, App
1484	30.4	4.0	15373	15	US-10-311-455-439	Sequence 439, App
1485	30.4	4.0	15387	15	US-10-311-455-158	Sequence 158, App
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OM nucleic - nucleic search, using sw model

Run on: January 24, 2005, 18:16:31 ; Search time 2066 Seconds
(without alignments)
13510.569 Million cell updates/sec

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database :

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7: gb_est6: *
8: gb_gss1: *
9: gb_gss2: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	671.8	87.7	856	7	CO581327 ILLUMIGEN
4	647.4	84.5	907	7	CO582275 ILLUMIGEN
5	642.6	83.9	924	7	CO644900 ILLUMIGEN
6	634.6	82.8	1006	4	BM923940 AGENCOURT
7	610.2	79.7	896	7	CO582384 ILLUMIGEN
8	496	64.8	713	7	CN793461 ILLUMIGEN
9	493.6	64.4	888	7	CO580240 ILLUMIGEN
10	492.2	64.3	705	7	CN786443 ILLUMIGEN
11	487.2	63.6	726	7	CN837742 ILLUMIGEN
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C 99	39.4	5.1	1128	7	CF596976	CF596976	AGENCOURT	C 172	36	4.7	149	5	BX255782	BX255782	BX255782
C 100	39.2	5.1	281	2	BB516670	BB516670	BB516670	C 173	36	4.7	252	2	BB036514	BB036514	BB036514
C 101	39.2	5.1	291	2	BB375714	BB375714	BB375714	C 174	36	4.7	266	2	BB006979	BB006979	BB006979
C 102	39.2	5.1	578	1	AI725209	AI725209	AI725209	C 175	36	4.7	283	1	AV325550	AV325550	AV325550
C 103	39	5.1	453	2	AW703939	AW703939	sk14a06.y	C 176	36	4.7	332	2	BB115991	BB115991	BB115991
C 104	39	5.1	478	7	CN792346	CN792346	4127194.B	C 177	36	4.7	471	4	BJ094908	BJ094908	BJ094908
C 105	39	5.1	1204	9	CNS016E2	AL106628	Drosophil	C 178	36	4.7	545	5	BY470456	BY470456	BY470456
C 106	38.8	5.1	613	4	BJ407375	BJ407375	BJ407375	C 179	36	4.7	690	8	BH208184	BH208184	BH208184
C 107	38.8	5.1	671	5	BX302895	BX302895	BX302895	C 180	36	4.7	815	9	CG974124	CG974124	CG974124
C 108	38.8	5.1	814	4	BG784777	BG784777	SEAUMC004	C 181	36	4.7	826	7	CN182549	CN182549	UCRCS04.0
C 109	38.2	5.0	570	6	CF312664	CF312664	ABF--08-I	C 182	36	4.7	1080	9	CNS00EPP	AL069494	Drosophil
C 110	38.2	5.0	648	2	AW497882	AW497882	660041C04	C 183	36	4.7	1201	9	CNS0107R	AL098625	Drosophil
C 111	38.2	5.0	671	5	BX866069	BX866069	BX866069	C 184	35.8	4.7	500	1	AV930455	AV930455	AV930455
C 112	38.2	5.0	766	5	BX861486	BX861486	BX861486	C 185	35.8	4.7	751	4	BI888233	BI888233	ZF637-1-0
C 113	38.2	5.0	789	5	BX302266	BX302266	BX302266	C 186	35.8	4.7	765	8	AQ935034	AQ935034	CpG2379A
C 114	38.2	5.0	866	6	CB633487	CB633487	OSIIEb12F	C 187	35.8	4.7	810	8	AQ935014	AQ935014	CpG2369A
C 115	38	5.0	688	7	CO080632	CO080632	GR_Ea44D	C 188	35.8	4.7	896	8	AZ674070	AZ674070	ENTKK22TF
C 116	38	5.0	937	9	CNS0207W	AL206357	Tetraodon	C 189	35.8	4.7	2721	3	AK090149	AK090149	Mus muscu
C 117	37.6	4.9	135	5	BX249501	BX249501	BX249501	C 190	35.6	4.6	324	5	BX689205	BX689205	BX689205
C 118	37.6	4.9	285	2	BB074742	BB074742	BB074742	C 191	35.6	4.6	470	6	CF096856	CF096856	QHN2F22.Y
C 119	37.6	4.9	363	1	AA279774	AA279774	zs92e09.B	C 192	35.6	4.6	504	8	AZ165656	AZ165656	SP_0082.B
C 120	37.6	4.9	376	5	BX254242	BX254242	BX254242	C 193	35.6	4.6	523	2	AW648555	AW648555	EST327009
C 121	37.6	4.9	377	5	BX249146	BX249146	BX249146	C 194	35.6	4.6	549	4	BJ221482	BJ221482	BJ221482
C 122	37.6	4.9	377	5	BX250874	BX250874	BX250874	C 195	35.6	4.6	638	6	CB681060	CB681060	OSJNEf06N
C 123	37.6	4.9	449	5	BX254094	BX254094	BX254094	C 196	35.6	4.6	639	9	CL659965	CL659965	PR10135d
C 124	37.6	4.9	798	5	BU852143	BU852143	AGENCOURT	C 197	35.6	4.6	674	9	AG124666	AG124666	Pan trogl
C 125	37.4	4.9	232	8	B58259	B58259	CIT-HSP-201	C 198	35.6	4.6	683	4	BJ714182	BJ714182	BJ714182
C 126	37.4	4.9	532	8	AQ178439	AQ178439	HS_2223.A	C 199	35.6	4.6	737	5	BU144245	BU144245	BU144245
C 127	37.4	4.9	815	9	CC592084	CC592084	CH240_392	C 200	35.6	4.6	807	9	AG165651	AG165651	Pan trogl
C 128	37.4	4.9	1009	9	CL135224	CL135224	ISH1-I06D	C 201	35.6	4.6	833	5	BU113228	BU113228	603130203
C 129	37.4	4.9	1101	9	CNS00B4E	AL056409	Drosophil	C 202	35.6	4.6	952	2	BE541205	BE541205	601064068
C 130	37.4	4.9	1571	8	CC189486	CC189486	CH261-36F	C 203	35.6	4.6	1061	9	AG382614	AG382614	Mus muscu
C 131	37.2	4.9	446	6	CF097240	CF097240	QHN3I18.Y	C 204	35.4	4.6	299	2	BB552635	BB552635	BB552635
C 132	37.2	4.9	525	6	CF096471	CF096471	QHN23E21.	C 205	35.4	4.6	400	4	BJ415704	BJ415704	BJ415704
C 133	37.2	4.9	589	6	CB489888	CB489888	omykrtfh0	C 206	35.4	4.6	507	2	BF517773	BF517773	NXSI_031
C 134	37.2	4.9	625	4	BJ501925	BJ501925	BJ501925	C 207	35.4	4.6	603	1	AI067971	AI067971	EST209660
C 135	37.2	4.9	640	6	CB489716	CB489716	omykrtfh0	C 208	35.4	4.6	645	1	AI166689	AI166689	xylem.est
C 136	37.2	4.9	747	5	BX081390	BX081390	BX081390	C 209	35.4	4.6	839	1	AV400694	AV400694	AV400694
C 137	37	4.8	459	1	AL819077	AL819077	AL819077	C 210	35.4	4.6	860	8	AZ680660	AZ680660	ENTGX30TR
C 138	37	4.8	583	6	CA844793	CA844793	hab91e03.	C 211	35.4	4.6	922	2	BE543834	BE543834	601071514
C 139	37	4.8	686	1	AL962933	AL962933	Arabidops	C 212	35.4	4.6	967	9	CL064547	CL064547	CH216-102
C 140	37	4.8	725	9	AJ589115	AJ589115	AJ589115	C 213	35.4	4.6	1101	9	CNS00EHN	AL069204	Drosophil
C 141	37	4.8	860	8	AQ741470	AQ741470	HS_5571.B	C 214	35.2	4.6	267	5	BX504843	BX504843	DKFZp686M
C 142	36.8	4.8	864	8	CC098399	CC098399	CSU-X34.1	C 215	35.2	4.6	533	8	AQ486354	AQ486354	RPCI-11-2
C 143	36.8	4.8	1059	9	CL014259	CL014259	ZMMBBb054	C 216	35.2	4.6	543	9	CR006073	CR006073	Forward s
C 144	36.8	4.8	1230	1	AU301029	AU301029	AU301029	C 217	35.2	4.6	582	8	AQ855803	AQ855803	CpG1627A
C 145	36.6	4.8	363	1	AI438356	AI438356	SWOVAFCAP	C 218	35.2	4.6	621	8	AZ523380	AZ523380	218PbF11
C 146	36.6	4.8	371	1	AT002520	AT002520	AT002520	C 219	35.2	4.6	689	7	CF517318	CF517318	CAP0005_I
C 147	36.6	4.8	401	5	BX501776	BX501776	DKFZp779O	C 220	35.2	4.6	690	9	CR034409	CR034409	Forward s
C 148	36.6	4.8	491	2	BF228854	BF228854	QC64a10.b	C 221	35.2	4.6	733	9	CR140345	CR034409	Forward s
C 149	36.6	4.8	533	5	BQ793354	BQ793354	EST_2292	C 222	35.2	4.6	778	9	BX997368	CR140345	Forward s
C 150	36.6	4.8	592	2	BE595816	BE595816	PI1_54.D1	C 223	35.2	4.6	780	9	CR027870	CR027870	Forward s
C 151	36.6	4.8	642	4	BM079639	BM079639	MEST97-D0	C 224	35.2	4.6	781	5	BX870144	BX870144	Forward s
C 152	36.6	4.8	699	6	CA079235	CA079235	SCSBAM108	C 225	35.2	4.6	782	9	BX984820	BX984820	Forward s
C 153	36.6	4.8	702	6	CA264459	CA264459	SCQGLB204	C 226	35.2	4.6	844	9	CR148016	CR148016	Forward s
C 154	36.6	4.8	808	9	CR242329	CR242329	Reverse s	C 227	35.2	4.6	861	5	BU938050	BU938050	AGENCOURT
C 155	36.6	4.8	963	3	AY105617	AY105617	Zea mays	C 228	35.2	4.6	864	9	CNS00BZ9	AL058529	Drosophil
C 156	36.6	4.8	1358	5	CL022089	CL022089	CH216-13K	C 229	35.2	4.6	865	9	CR179050	CR179050	Forward s
C 157	36.4	4.8	626	5											

C 244	35	4.6	681	9	CR001380	CR001380 Forward s	317	34.6	4.5	457	7	T88391	T88391 12087 Lambd
245	35	4.6	791	6	CD776245	UI-M-AQ0-	C 318	34.6	4.5	528	4	BI128486	BI128486 G076P74Y
246	35	4.6	791	9	BX209122	Danio rer	C 319	34.6	4.5	555	7	CK102412	CK102412 G076P74.5
247	35	4.6	795	8	BH603746	BOGEL51TR	320	34.6	4.5	571	5	BU778992	BU778992 SJEESC02
C 248	35	4.6	830	8	CC109681	NDL.29P17	321	34.6	4.5	615	6	CA926534	CA926534 MTU6CR.P1
249	35	4.6	1509	3	CNS0A9PM	BX820895 Arabidops	C 322	34.6	4.5	617	9	CE700116	CE700116 tigr-g88-
250	35	4.6	1526	3	CNS0A9KO	BX820563 Arabidops	323	34.6	4.5	637	4	BG974431	BG974431 602844212
C 251	35	4.6	2142	3	AK031184	Mus muscu	324	34.6	4.5	642	4	BG973919	BG973919 602843555
C 252	34.8	4.5	277	4	BG098616	BG098616 EST463135	325	34.6	4.5	658	5	BX252728	BX252728 BX252728
C 253	34.8	4.5	291	1	AV338652	AV338652	326	34.6	4.5	666	4	BI661990	BI661990 603304985
C 254	34.8	4.5	293	2	BB721081	BB721081	327	34.6	4.5	681	4	BG861503	BG861503 602795465
255	34.8	4.5	294	5	BQ451988	BQ451988 PFESToaa9	328	34.6	4.5	681	4	BG915006	BG915006 602813879
C 256	34.8	4.5	333	5	BU701801	BU701801 UI-M-F10-	329	34.6	4.5	689	4	BI662480	BI662480 603304472
C 257	34.8	4.5	363	6	CD545065	CD545065 B0264A02-	C 330	34.6	4.5	695	9	AG001435	AG001435 Homo sapi
258	34.8	4.5	391	5	BQ149628	BQ149628 NF107A11F	331	34.6	4.5	707	8	BH980005	BH980005 odfo1e07.
C 259	34.8	4.5	426	7	CN699164	CN699164 E0417G08-	332	34.6	4.5	712	4	BG863366	BG863366 602797005
C 260	34.8	4.5	439	7	CF903111	CF903111 A0400C09-	C 333	34.6	4.5	722	5	BP461634	BP461634 BP461634
C 261	34.8	4.5	442	8	B78782	CIT-HSP-616	334	34.6	4.5	723	5	BX309208	BX309208 BX309208
C 262	34.8	4.5	480	6	CF168185	CF168185 B0795F09-	335	34.6	4.5	729	5	BQ580323	BQ580323 ACB89-jm1
C 263	34.8	4.5	487	6	CF167827	CF167827 B0790F04-	336	34.6	4.5	735	4	BI656976	BI656976 603284594
C 264	34.8	4.5	501	6	CA557216	CA557216 K0224A09-	C 337	34.6	4.5	735	5	BX746817	BX746817 BX746817
C 265	34.8	4.5	501	9	CL721921	CL721921 OR_BBA005	C 338	34.6	4.5	738	5	BP459092	BP459092 BP459092
C 266	34.8	4.5	502	7	CK393020	CK393020 K0853B08-	339	34.6	4.5	741	4	BI853687	BI853687 603380827
C 267	34.8	4.5	508	7	CN705083	CN705083 E0496F08-	340	34.6	4.5	755	4	BG975001	BG975001 602843412
C 268	34.8	4.5	510	7	CN667348	CN667348 A0852C07-	341	34.6	4.5	755	9	CE218122	CE218122 tigr-g88-
C 269	34.8	4.5	512	6	CD538284	CD538284 B0201G09-	342	34.6	4.5	756	4	BI660212	BI660212 603302579
C 270	34.8	4.5	517	7	CN700974	CN700974 E043C08-	343	34.6	4.5	756	9	CC568180	CC568180 CH240.442
C 271	34.8	4.5	519	2	BF113440	BF113440 EST441030	344	34.6	4.5	760	4	BI657811	BI657811 603284617
C 272	34.8	4.5	522	6	CF167867	CF167867 B0791B07-	345	34.6	4.5	770	4	BI656261	BI656261 603283049
C 273	34.8	4.5	523	7	CN692328	CN692328 E0321D05-	346	34.6	4.5	778	4	BG861708	BG861708 602795292
C 274	34.8	4.5	530	6	CD546447	CD546447 B0274B05-	C 347	34.6	4.5	782	7	CN520527	CN520527 GQ0107.B3
C 275	34.8	4.5	533	7	CN692711	CN692711 E0326G01-	348	34.6	4.5	788	4	BI654515	BI654515 603281901
276	34.8	4.5	543	5	BQ835038	BQ835038 Po ad 06E	349	34.6	4.5	800	4	BI655730	BI655730 603281325
C 277	34.8	4.5	550	7	CN696471	CN696471 E0379H04-	350	34.6	4.5	821	4	BI655297	BI655297 603283320
C 278	34.8	4.5	553	6	CF164817	CF164817 B0748C03-	351	34.6	4.5	853	4	BI657228	BI657228 603282904
279	34.8	4.5	606	7	CO118046	CO118046 GR_Eb020	352	34.6	4.5	877	8	AQ856793	AQ856793 nbeb0004K
C 280	34.8	4.5	608	5	BQ560211	BQ560211 H4062H10-	C 353	34.6	4.5	904	9	CC872533	CC872533 NDL.118B2
C 281	34.8	4.5	625	7	CF915409	CF915409 B0979D07-	354	34.6	4.5	908	4	BI655773	BI655773 603281375
C 282	34.8	4.5	641	7	CF915058	CF915058 B0973E03-	355	34.6	4.5	925	9	CNS04KMP	AL295018 Tetraodon
C 283	34.8	4.5	657	7	CK390520	CK390520 K0820A11-	356	34.6	4.5	1000	4	BI656544	BI656544 603285987
C 284	34.8	4.5	668	7	CK392685	CK392685 K0848G06-	357	34.6	4.5	1101	9	CNS0100X	AL098379 Drosophi1
C 285	34.8	4.5	671	5	BQ745402	BQ745402 UI-M-EW0-	358	34.6	4.5	1103	4	BG861866	BG861866 602794817
C 286	34.8	4.5	686	7	CK633779	CK633779 UI-M-HN0-	C 359	34.4	4.5	256	1	AV276642	AV276642 AV276642
287	34.8	4.5	689	1	AV385901	AV385901 AV385901	C 360	34.4	4.5	265	7	CF612604	CF612604 lae13C11.
C 288	34.8	4.5	691	7	CN454780	CN454780 UI-M-HN0-	C 361	34.4	4.5	266	7	CF352876	CF352876 lab50C07.
C 289	34.8	4.5	693	6	CB244551	CB244551 UI-M-FY0-	C 362	34.4	4.5	266	7	CF755092	CF755092 lae52h12.
C 290	34.8	4.5	694	7	CN537967	CN537967 UI-M-HS0-	C 363	34.4	4.5	267	7	CF968907	CF968907 lag74e08.
C 291	34.8	4.5	706	5	BM964142	BM964142 UI-M-EQ0-	C 364	34.4	4.5	279	7	CK384136	CK384136 lah02h05.
C 292	34.8	4.5	715	6	CB245343	CB245343 UI-M-FY0-	C 365	34.4	4.5	280	7	CF612108	CF612108 lae28a03.
C 293	34.8	4.5	722	6	CB525667	CB525667 UI-M-FY0-	C 366	34.4	4.5	283	7	CF352989	CF352989 lab50C04.
C 294	34.8	4.5	732	7	CK639584	CK639584 UI-M-HN0-	C 367	34.4	4.5	285	7	CK374159	CK374159 lai57d10.
C 295	34.8	4.5	739	6	CB521908	CB521908 UI-M-GH0-	C 368	34.4	4.5	286	2	BB090521	BB090521 BB090521
C 296	34.8	4.5	742	6	CB244185	CB244185 UI-M-FY0-	C 369	34.4	4.5	287	2	BB141202	BB141202 BB141202
C 297	34.8	4.5	751	7	CK635957	CK635957 UI-M-HN0-	C 370	34.4	4.5	288	7	CF545042	CF545042 laq86h01.
C 298	34.8	4.5	751	7	CO101715	CO101715 GR_Eb002	371	34.4	4.5	289	5	BX254614	BX254614 BX254614
C 299	34.8	4.5	755	9	CNS020HE	AL175595 Tetraodon	C 372	34.4	4.5	297	2	BB025145	BB025145 BB025145
300	34.8	4.5	771	7	CO101866	CO101866 GR_Eb002	C 373	34.4	4.5	299	2	BB366155	BB366155 BB366155
C 301	34.8	4.5	772	6	CA764724	CA764724 AF53-Rpf	C 374	34.4	4.5	300	2	BB211801	BB211801 BB211801
C 302	34.8	4.5	775	7	CO086468	CO086468 GR_Ea04H	C 375	34.4	4.5	300	2	BB298714	BB298714 BB298714
C 303	34.8	4.5	789	7	CF668769	CF668769 RTCTNT1.38	C 376	34.4	4.5	301	1	AV347881	AV347881 AV347881
C 304	34.8	4.5	815	6	CB244766	CB244766 UI-M-FY0-	C 377	34.4	4.5	305	1	AV348624	AV348624 AV348624
C 305	34.8	4.5	823	7	CN531568	CN531568 UI-M-HQ0-	C 378	34.4	4.5	322	1	AV318704	AV318704 AV318704
C 306	34.8	4.5	853	8	BH584567	BH584567 BOGFV09TR	C 379	34.4	4.5	323	2	BB070791	BB070791 BB070791
307	34.8	4.5	865	8	BZ172638	BZ172638 CH230-369	C 380	34.4	4.5	329	2	BE956586	BE956586 UI-M-BG2-
308	34.8	4.5	878	6	CB208450	CB208450 AGENCOURT	381	34.4	4.5	330	2	AW121527	AW121527 UI-M-BH2.
C 309	34.8	4.5	885	4	BI656076	BI656076 603284735	C 382	34.4	4.5	331	2	BB392044	BB392044 BB392044
310	34.8	4.5	942	9	CNS02294	AL220657 Tetraodon	C 383	34.4	4.5	332	2	BB793509	BB793509 BB793509
C 311	34.8	4.5	978	3	CR713554	CR713554 Tetraodon	384	34.4	4.5	350	2	AW240480	AW240480 uq35d07.x
C 312	34.8	4.5	1098	9	CC932661	CC932661 ZMMBbc054	C 385	34.4	4.5	379	2	BB738128	BB738128 BB738128
C 313	34.8	4.5	1130	9	CNS02WBD	AL216742 Tetraodon	C 386	34.4	4.5	382	2	BB738074	BB738074 BB738074
314	34.6	4.5	323	6	CD699634	CD699634 EST16030	C 387	34.4	4.5	382	7	CK377808	CK377808 lai089l0.
315	34.6	4.5	394	8	AQ241575	AQ241575 CITBI-E1-	C 388	34.4	4.5	387	4	BM124429	BM124429 L0539H12-
316	34.6	4.5	430	7	CO722365	CO722365 MdfR3019n	C 389	34.4	4.5	393	6	BY642121	BY642121 BY642121

C 390	34.4	4.5	419	2	BB742345
C 391	34.4	4.5	423	2	BB826487
C 392	34.4	4.5	429	6	CA876962
C 393	34.4	4.5	439	4	BJ065493
C 394	34.4	4.5	451	2	BB770395
C 395	34.4	4.5	457	1	AI118573
C 396	34.4	4.5	457	1	AI118573
C 397	34.4	4.5	458	6	BD710397
C 398	34.4	4.5	465	2	BB744930
C 399	34.4	4.5	472	4	BM146485
C 400	34.4	4.5	472	8	AQ479756
C 401	34.4	4.5	478	2	BB829859
C 402	34.4	4.5	483	1	AI315295
C 403	34.4	4.5	487	1	BB762298
C 404	34.4	4.5	498	2	AI957077
C 405	34.4	4.5	499	8	AZ517364
C 406	34.4	4.5	500	2	AW763553
C 407	34.4	4.5	500	2	BF017898
C 408	34.4	4.5	508	2	AW610767
C 409	34.4	4.5	508	6	CD540697
C 410	34.4	4.5	510	1	AI461967
C 411	34.4	4.5	514	2	BB763133
C 412	34.4	4.5	514	2	BB764583
C 413	34.4	4.5	516	5	BY466523
C 414	34.4	4.5	523	6	CD707517
C 415	34.4	4.5	525	2	BB764443
C 416	34.4	4.5	532	2	BB769183
C 417	34.4	4.5	534	2	BB768928
C 418	34.4	4.5	563	4	BI105752
C 419	34.4	4.5	576	5	BP766948
C 420	34.4	4.5	582	4	BI477179
C 421	34.4	4.5	582	6	CD684058
C 422	34.4	4.5	583	5	BP768864
C 423	34.4	4.5	587	9	CG952461
C 424	34.4	4.5	589	5	BP766884
C 425	34.4	4.5	597	5	BP757053
C 426	34.4	4.5	603	8	AQ459573
C 427	34.4	4.5	605	4	BI477202
C 428	34.4	4.5	611	5	BY479578
C 429	34.4	4.5	620	6	CD690618
C 430	34.4	4.5	623	6	CD683742
C 431	34.4	4.5	647	4	BJ065840
C 432	34.4	4.5	647	6	CB507035
C 433	34.4	4.5	689	8	BH945418
C 434	34.4	4.5	694	8	AZ869901
C 435	34.4	4.5	717	5	BU203953
C 436	34.4	4.5	724	6	CF283043
C 437	34.4	4.5	735	8	BZ057573
C 438	34.4	4.5	774	9	CR079959
C 439	34.4	4.5	846	7	CF836623
C 440	34.4	4.5	897	7	CK798587
C 441	34.4	4.5	902	6	CB198161
C 442	34.4	4.5	909	8	AF011186
C 443	34.4	4.5	915	9	CL040341
C 444	34.4	4.5	946	9	CL016927
C 445	34.4	4.5	970	9	CNS02KVM
C 446	34.4	4.5	1010	9	CL039923
C 447	34.4	4.5	1028	9	CL034284
C 448	34.4	4.5	1045	9	CL079107
C 449	34.4	4.5	1050	9	CNS04EA3
C 450	34.4	4.5	1057	9	CL029984
C 451	34.4	4.5	1064	9	CL034555
C 452	34.4	4.5	1086	9	CL016831
C 453	34.4	4.5	1196	9	CL104968
C 454	34.2	4.5	275	2	BE702156
C 455	34.2	4.5	275	4	BI962355
C 456	34.2	4.5	401	8	AZ226964
C 457	34.2	4.5	450	5	BQ128791
C 458	34.2	4.5	483	1	AA733437
C 459	34.2	4.5	503	4	BJ467184
C 460	34.2	4.5	513	5	BP656183
C 461	34.2	4.5	534	4	BJ467249
C 462	34.2	4.5	549	9	CL312916

C 463	34.2	4.5	552	6	CA016927
C 464	34.2	4.5	563	9	CE461481
C 465	34.2	4.5	637	9	AG014550
C 466	34.2	4.5	655	7	CN135161
C 467	34.2	4.5	660	9	CL750932
C 468	34.2	4.5	672	6	CD394634
C 469	34.2	4.5	694	1	AV920760
C 470	34.2	4.5	696	4	BJ734675
C 471	34.2	4.5	700	2	BE876198
C 472	34.2	4.5	716	8	BH110294
C 473	34.2	4.5	726	6	BY765148
C 474	34.2	4.5	733	6	CF270923
C 475	34.2	4.5	741	9	AX142905
C 476	34.2	4.5	743	7	CN135234
C 477	34.2	4.5	788	7	CF391770
C 478	34.2	4.5	799	9	CC812405
C 479	34.2	4.5	833	9	CL671547
C 480	34.2	4.5	834	2	BF675136
C 481	34.2	4.5	840	8	BZ816570
C 482	34.2	4.5	883	9	CG464206
C 483	34.2	4.5	939	9	CL470056
C 484	34.2	4.5	1018	8	CC255799
C 485	34.2	4.5	1558	3	CNS0A9EJ
C 486	34	4.4	324	1	AI835944
C 487	34	4.4	409	8	AZ004640
C 488	34	4.4	414	8	AZ094701
C 489	34	4.4	493	8	AZ410718
C 490	34	4.4	516	5	BU476821
C 491	34	4.4	517	5	BU476728
C 492	34	4.4	526	8	CC410978
C 493	34	4.4	578	5	BU496612
C 494	34	4.4	593	2	AW533498
C 495	34	4.4	596	8	BH173518
C 496	34	4.4	604	5	BU495658
C 497	34	4.4	609	1	AI490152
C 498	34	4.4	611	7	CN538312
C 499	34	4.4	615	6	CA329922
C 500	34	4.4	623	1	AI057980
C 501	34	4.4	626	5	BQ204059
C 502	34	4.4	631	8	AZ467632
C 503	34	4.4	647	9	CG945014
C 504	34	4.4	655	8	BH882460
C 505	34	4.4	661	8	AZ348411
C 506	34	4.4	664	9	CG706616
C 507	34	4.4	670	8	BZ324568
C 508	34	4.4	674	8	AQ969808
C 509	34	4.4	676	9	CL747571
C 510	34	4.4	687	4	BG128443
C 511	34	4.4	688	4	BG130642
C 512	34	4.4	698	9	CR033761
C 513	34	4.4	715	7	CN538407
C 514	34	4.4	719	9	AG137836
C 515	34	4.4	755	8	BZ620740
C 516	34	4.4	768	9	AG184404
C 517	34	4.4	769	9	AG469514
C 518	34	4.4	804	7	CN054476
C 519	34	4.4	826	8	BZ222801
C 520	34	4.4	893	5	BQ222536
C 521	34	4.4	919	8	AZ545468
C 522	34	4.4	995	9	CNS016WR
C 523	34	4.4	1051	8	CC246743
C 524	34	4.4	1058	9	CNS04TND
C 525	34	4.4	1102	9	CNS0152I
C 526	33.8	4.4	338	1	AI724183
C 527	33.8	4.4	349	6	CA770616
C 528	33.8	4.4	356	1	AU276935
C 529	33.8	4.4	425	5	BX721215
C 530	33.8	4.4	434	4	BI746750
C 531	33.8	4.4	477	8	AQ642250
C 532	33.8	4.4	480	8	AQ053239
C 533	33.8	4.4	483	9	CR499096
C 534	33.8	4.4	488	5	BU813635
C 535	33.8	4.4	513	8	BZ870333

CA016927	HV05J11u
CE461481	tigr-gss-
AG014550	Homo sapi
CN135161	OX1_31_A1
CL750932	OR_BBa011
CD394634	GR_ck1437
AV920760	AV920760
BJ734675	BJ734675
BE876198	601486718
BH110294	RPCI-24-2
BY765148	BY765148
CF270923	AGENCOURT
AX142905	Danio rer
CN135234	OX1_31_A1
CF391770	RTDR3_11
CC812405	ZMMBBC052
CL671547	PR10165a
BF675136	602136541
BZ816570	PUF4V10TB
CG464206	ZUAHM05TH
CL470056	SAIL_138
CC255799	CH261_161
BX819886	Arabidops
AI835944	UI-M-AI0-
AZ004640	RPCI-23-3
AZ094701	RPCI-23-4
AZ410718	IM0183P09
BU476821	603847164
BU476728	603468680
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AW533498	UI-R-BU0-
BH173518	Gm_ISB001
BU495658	PfESToab7
AI490152	EST246744
CN538312	UI-M-HS0-
CA329922	hablla08.
AI057980	SWOVL3CAN
BQ204059	UI-R-DN1-
AZ467632	1M0279G10
CG945014	MBEIN71TF
BH882460	hw37e03.9
AZ348411	1M0084I20
CG706616	BARC_BFGL
BZ324568	ic11d04.9
AQ969808	LERJQ52TF
CL747571	OR_BBa011
BG128443	EST474089
BG130642	EST476269
CR033761	Forward s
CN538407	UI-M-HS0-
AG137836	Pan trogl
BZ620740	ig67f05.b
AG184404	Pan trogl
AG469514	Mus muscu
CN054476	Salamande
BZ222801	CH230-260
BQ222536	AGENCOURT
AZ545468	ENTGD40TR
AL107301	Drosophil
CC246743	CH261-187
AL104916	Tetraodon
AL104916	Drosophil
AI724183	RHIZ1_8_B
CA770616	ssalssha00
AU276935	AU276935
BX721215	BX721215
BI746750	rm31c07.Y
AQ642250	RPCI93-EC
AQ053239	CIT-HSP-2
CR499096	Medicago
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BZ870333	CH240_289

536	33.8	4.4	532	8	AQ336448	HS_5017_B	AQ336448	HS_5017_B
C 537	33.8	4.4	538	9	TA200F12Q		AL479212	T_brucel
C 538	33.8	4.4	555	1	AI067999		AI067999	EST209688
C 539	33.8	4.4	561	4	BJ222730		BJ222730	BJ222730
C 540	33.8	4.4	602	8	BH032088		BH032088	RPCI-24-3
C 541	33.8	4.4	648	2	AW375610	QV0-CT017	AW375610	QV0-CT017
542	33.8	4.4	648	2	AW498070		AW498070	660041C04
543	33.8	4.4	649	1	AJ803785		AJ803785	AJ803785
C 544	33.8	4.4	653	1	AI067214		AI067214	EST208888
C 545	33.8	4.4	663	1	AI067933	EST209621	AI067933	EST209621
546	33.8	4.4	663	9	CG954848		CG954848	MBEAM41TF
547	33.8	4.4	672	1	AJ803102		AJ803102	AJ803102
548	33.8	4.4	676	9	CL313990	meth2-130N	CL313990	meth2-130N
C 549	33.8	4.4	695	5	BU813117		BU813117	N005E02_P
C 550	33.8	4.4	703	7	CN853978		CN853978	Ha_mx0_19
551	33.8	4.4	711	7	CF478402		CF478402	RTW3_18
C 552	33.8	4.4	726	5	BU884566		BU884566	R012D07_P
C 553	33.8	4.4	729	7	CK109741		CK109741	N021B05_P
C 554	33.8	4.4	738	6	CB311718		CB311718	AGENCOURT
555	33.8	4.4	742	6	CA057347		CA057347	ssailrgb53
556	33.8	4.4	747	9	CNS00922		AL054517	Drosophil
557	33.8	4.4	755	7	CF923359		CF923359	ML_MQ1_06
C 558	33.8	4.4	774	5	BW166560		BW166560	BW166560
C 559	33.8	4.4	778	9	CR095245	Reverse s	CR095245	Reverse s
C 560	33.8	4.4	790	8	BH040645	RPCI-24-3	BH040645	RPCI-24-3
C 561	33.8	4.4	793	8	BH575837		BH575837	BOGBQ82TF
C 562	33.8	4.4	809	7	CN584950		CN584950	USDA-FP_1
C 563	33.8	4.4	812	5	BU812937		BU812937	N003B12_P
564	33.8	4.4	837	7	CO574783		CO574783	AGENCOURT
C 565	33.8	4.4	842	4	BM397496		BM397496	S009-0-33
566	33.8	4.4	845	7	CO199220		CO199220	GE01_19_D
567	33.8	4.4	876	7	CO198154		CO198154	GE01_11_D
568	33.8	4.4	880	5	BX739977		BX739977	BX739977
C 569	33.8	4.4	881	5	BX739973		BX739973	BX739973
570	33.8	4.4	884	4	BG433065		BG433065	602496804
571	33.8	4.4	898	8	AZ528384		AZ528384	ENTBY21TR
C 572	33.8	4.4	904	8	AZ546660		AZ546660	ENTFQ22TF
C 573	33.8	4.4	905	9	CNS00F72		AL070220	Drosophil
574	33.8	4.4	914	9	CG919472		CG919472	MBEMJ54TR
575	33.8	4.4	942	8	BH157632		BH157632	ENTSV32TF
576	33.8	4.4	973	8	AZ670650		AZ670650	ENTHC61TF
C 577	33.8	4.4	1101	9	CNS00F30		AL071298	Drosophil
578	33.6	4.4	202	6	CA317230	UI-M-FW0-	CA317230	UI-M-FW0-
579	33.6	4.4	279	2	BE058564		BE058564	sn17g09.Y
C 580	33.6	4.4	328	1	AU261705		AU261705	AU261705
C 581	33.6	4.4	354	5	BQ602703	MI-P-NA-a	BQ602703	MI-P-NA-a
C 582	33.6	4.4	395	5	BP633395		BP633395	BP633395
C 583	33.6	4.4	405	5	BP660013		BP660013	BP660013
584	33.6	4.4	412	8	BZ671900		BZ671900	PUBIC31TD
C 585	33.6	4.4	422	5	BU031097		BU031097	QHJ17G20.
C 586	33.6	4.4	451	8	BH491945		BH491945	BOHMR03TF
587	33.6	4.4	473	8	AZ518814	RPCI-11-3	AZ518814	RPCI-11-3
588	33.6	4.4	482	8	AQ129455	HS_3045_A	AQ129455	HS_3045_A
C 589	33.6	4.4	500	7	CF405836		CF405836	CSECS059H
C 590	33.6	4.4	503	5	BQ602443	MI-P-NA-a	BQ602443	MI-P-NA-a
591	33.6	4.4	547	8	AQ782708		AQ782708	HS_5327_A
C 592	33.6	4.4	552	7	CK572012	est_l_van	CK572012	est_l_van
C 593	33.6	4.4	568	6	CB982247		CB982247	CAB70006
C 594	33.6	4.4	581	4	BJ181221		BJ181221	BJ181221
595	33.6	4.4	594	8	BH719437		BH719437	BOWKK04TF
C 596	33.6	4.4	611	6	CF213145		CF213145	CGF100063
597	33.6	4.4	626	6	CD980922		CD980922	QAI18e02.
C 598	33.6	4.4	648	9	AG071384		AG071384	Pan trogl
C 599	33.6	4.4	663	8	BH177905	010_D_16-	BH177905	010_D_16-
C 600	33.6	4.4	663	9	CNS07KCC		AL614862	T3_end of
601	33.6	4.4	686	8	BZ088224		BZ088224	lkx77a03.
C 602	33.6	4.4	696	6	CB290690		CB290690	UCRCS01_0
603	33.6	4.4	696	6	CD648250	AUF_102_E	CD648250	AUF_102_E
604	33.6	4.4	724	9	CNS00DLE		AL071881	Drosophil
605	33.6	4.4	726	9	CE455490		CE455490	tigr-g88-
606	33.6	4.4	741	4	BG696490	602658810	BG696490	602658810
607	33.6	4.4	780	9	CC872657	NDL.22E13	CC872657	NDL.22E13
608	33.6	4.4	824	8	BH354356	CH230-221	BH354356	CH230-221
CK090795	F025P39.3		835	7	CK090795		CK090795	
BX377559	BX377559	4.4	966	5	BX377559		BX377559	
BU541791	AGENCOURT	4.4	1020	5	BU541791		BU541791	
BB040102	BB040102	4.4	290	2	BB040102		BB040102	
AL006365	F_rubripe	4.4	436	9	FR0015156		FR0015156	
CG410561	gbs3_VM7	4.4	527	9	CG410561		CG410561	
BM432826	1JEJ6E10-	4.4	528	4	BM432826		BM432826	
CR573062	CR573062	4.4	547	7	CR573062		CR573062	
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BH301028	CH230-179	4.4	564	8	BH301028		BH301028	
AZ371157	1M0122B04	4.4	573	8	AZ371157		AZ371157	
AU238264	AU238264	4.4	579	1	AU238264		AU238264	
AZ948037	2M0210O22	4.4	587	8	AZ948037		AZ948037	
CN247408	EST013300	4.4	593	7	CN247408		CN247408	
CA728754	wd11c.pk0	4.4	604	6	CA728754		CA728754	
CN878644	020906AAR	4.4	604	7	CN878644		CN878644	
CL579090	OB_Ba003	4.4	613	9	CL579090		CL579090	
AQ377603	RPCI11-14	4.4	626	8	AQ377603		AQ377603	
AL340877	Tetraodon	4.4	629	9	CNS05KOK		CNS05KOK	
BH270084	CH230-6N1	4.4	646	8	BH270084		BH270084	
AJ789256	AJ789256	4.4	651	1	AJ789256		AJ789256	
CO603742	DG8-26811	4.4	670	1	AA020845		AA020845	
AA020845	ze64a07.r	4.4	692	1	AI729444		AI729444	
AI729444	BNLGH1133	4.4	718	8	BH926990		BH926990	
BH926990	odi21c10.	4.4	720	8	BH550487		BH550487	
BH550487	BOHKS40TF	4.4	740	9	CG676034		CG676034	
CG676034	tir3766.t	4.4	745	5	BX302265		BX302265	
BX302265	BX302265	4.4	755	8	AQ751371	HS_5575_B	AQ751371	HS_5575_B
AQ751371	HS_5575_B	4.4	757	5	BU363716		BU363716	
BU363716	603785288	4.4	768	8	CC343736		CC343736	
CC343736	OGUAP11TH	4.4	799	7	CNS07249		CNS07249	
CNS07249	AGENCOURT	4.4	821	7	CR563909		CR563909	
CR563909	CR563909	4.4	823	8	BZ746916		BZ746916	
BZ746916	PUCEQ77TD	4.4	848	5	BU325524	603490628	BU325524	603490628
BU325524	603490628	4.4	859	8	AZ689000		AZ689000	
AZ689000	ENTKB52TF	4.4	871	8	BH159288		BH159288	
BH159288	ENTSB26TF	4.4	893	8	AZ687955		AZ687955	
AZ687955	ENTHP59TF	4.4	894	8	AZ547012		AZ547012	
AZ547012	ENTEX58TR	4.4	895	8	BH146492		BH146492	
BH146492	ENTQL29TR	4.4	908	4	BG295613	602392995	BG295613	602392995
BG295613	602392995	4.4	918	8	AZ139584	SP_0158_A	AZ139584	SP_0158_A
AZ139584	SP_0158_A	4.4	924	8	AZ674562		AZ674562	
AZ674562	ENT116TF	4.4	931	5	BQ734031		BQ734031	
BQ734031	AGENCOURT	4.4	1101	9	CNS0039G		CNS0039G	
CNS0039G	Drosophil	4.4	1101	9	CNS012RM		CNS012RM	
AL101932	Drosophil	4.4	1273	3	CL027009		CL027009	
CL027009	CH216-24M	4.4	1534	3	CNS0A399		CNS0A399	
CNS0A399		4.4	1568	8	CC190488		CC190488	
CC190488	CH261-191	4.4	244	4	BG231287		BG231287	
BG231287	nah84g08.	4.3	246	4	BJ518573		BJ518573	
BJ518573	BJ518573	4.3	287	2	BB285429		BB285429	
BB285429	BB285429	4.3	302	4	BM535932	EST588954	BM535932	EST588954
BM535932	EST588954	4.3	319	9	CE199185	tigr-g88-	CE199185	tigr-g88-
CE199185	tigr-g88-	4.3	358	4	BG098618		BG098618	
BG098618	EST463137	4.3	368	7	CK714755		CK714755	
CK714755	LECAD01B1	4.3	371	4	BM413609		BM413609	
BM413609	EST587936	4.3	379	5	BX115736		BX115736	
BX115736	BX115736	4.3	387	1	AI778135		AI778135	
AI778135	EST259014	4.3	441	2	BB834287		BB834287	
BB834287	BB834287	4.3	447	4	BG233017		BG233017	
BG233017	daa31b09.	4.3	450	7	CR291575		CR291575	
CR291575	CR291575	4.3	454	5	BY508612		BY508612	
BY508612	BY508612	4.3	460	5	BP581349		BP581349	
BP581349	BP581349	4.3	468	1	AI778372		AI778372	
AI778372	EST259251	4.3	477	2	BE434470		BE434470	
BE434470	EST405548	4.3	500	6	CF163019		CF163019	
CF163019	EST19H05-	4.3	502	2	AW092191		AW092191	
AW092191	EST285287	4.3	503	6	CD552363	B0341F01-	CD552363	B0341F01-
CD552363	B0341F01-	4.3	510	7	CN683194		CN683194	
CN683194	E0175D01-	4.3	518	6	CF165485		CF165485	
CF165485	B0757D01-	4.3	519	8	AQ378907		AQ378907	
AQ378907	RPC111-16	4.3	521	6	CD554959		CD554959	
CD554959	B0384F05-	4.3						

C 682	33.2	4.3	522	6	CA870580	CA870580 K0903B09-	C 755	33	4.3	578	5	BU629298	UI-H-FL0-
C 683	33.2	4.3	522	6	CA875662	K0942F11-	C 756	33	4.3	588	4	BJ053905	BJ053905
C 684	33.2	4.3	530	4	BM413561	EST587888	C 757	33	4.3	589	7	CN633459	tafl1b02.
C 685	33.2	4.3	533	7	CN673974	A0942C06-	C 758	33	4.3	591	7	CO636433	USDA-FP_1
C 686	33.2	4.3	534	5	BQ167571	WHE0076 F	C 759	33	4.3	592	6	CF195241	USDA-FP_1
C 687	33.2	4.3	535	7	CN681771	E0155A06-	C 760	33	4.3	595	7	CF916477	B0995F09-
C 688	33.2	4.3	547	2	AW035331	EST280694	C 761	33	4.3	607	7	CO755397	Mdfrt3049
C 689	33.2	4.3	559	7	CN690119	E0289A03-	C 762	33	4.3	610	7	CN633206	tafl1b02.
C 690	33.2	4.3	574	8	AQ885296	HS 5522 B	C 763	33	4.3	611	5	BQ535624	STEM2_16
C 691	33.2	4.3	577	1	AI895551	EST264994	C 764	33	4.3	634	1	AL714497	AL714497
C 692	33.2	4.3	579	2	BF098441	EST428962	C 765	33	4.3	638	5	BU673239	NL_12_78
C 693	33.2	4.3	579	4	BI993480	01421 lea	C 766	33	4.3	638	7	CF914028	CF914028
C 694	33.2	4.3	591	9	CE175633	tigr-gss-	C 767	33	4.3	640	7	CF915804	B0985E03-
C 695	33.2	4.3	594	8	AQ026573	CIT-HSP-2	C 768	33	4.3	647	5	BQ594695	E012404-0
C 696	33.2	4.3	598	4	BM409794	EST584121	C 769	33	4.3	666	6	CF173148	B0919C08-
C 697	33.2	4.3	603	7	CN353420	CN353420 170006001	C 770	33	4.3	671	1	AL642221	AL642221
C 698	33.2	4.3	612	6	CA875331	K0939C02-	C 771	33	4.3	672	2	AW979365	EST310413
C 699	33.2	4.3	617	9	CE202502	tigr-gss-	C 772	33	4.3	676	8	BH956763	odh04d12.
C 700	33.2	4.3	619	2	AW934247	AW934247 EST462137	C 774	33	4.3	683	9	CL599760	OB_Ba006
C 701	33.2	4.3	635	4	BG097618	EST462137	C 775	33	4.3	691	5	BQ007955	UI-H-EI0-
C 702	33.2	4.3	642	6	CF308048	ABF--01-L	C 776	33	4.3	693	9	CL814014	OR_CBa003
C 703	33.2	4.3	646	6	CA879767	K0976F07-	C 777	33	4.3	696	8	AQ255734	nbxb0014C
C 704	33.2	4.3	647	9	CR299014	Medicago	C 778	33	4.3	701	1	AV783773	AV783773
C 705	33.2	4.3	660	4	BI935955	EST555844	C 779	33	4.3	701	9	AG339045	Mus muscu
C 706	33.2	4.3	660	8	AZ525389	AZ525389 243PbE04	C 780	33	4.3	702	8	BH736306	BOHYH25TF
C 707	33.2	4.3	664	8	AQ380827	RPC111-16	C 781	33	4.3	705	4	BG603336	EST502426
C 708	33.2	4.3	669	9	AG154904	Pan trogl	C 782	33	4.3	705	4	BG603336	EST502426
C 709	33.2	4.3	679	2	AW442803	EST307733	C 783	33	4.3	705	4	BM674718	UI-E-EJ0-
C 710	33.2	4.3	679	9	CL765303	CL765303 OR_BBa013	C 784	33	4.3	712	8	BZ074959	lk938f06.
C 711	33.2	4.3	685	9	CE048480	tigr-gss-	C 785	33	4.3	715	4	BI662482	603304474
C 712	33.2	4.3	700	9	AG001434	Homo sapi	C 786	33	4.3	733	8	BZ361823	ie25g04.b
C 713	33.2	4.3	731	7	CN754130	ID0AA12A	C 787	33	4.3	739	4	BG862087	602795622
C 714	33.2	4.3	779	9	CC485180	CH240_314	C 788	33	4.3	771	4	BI661001	603304092
C 715	33.2	4.3	779	8	AQ750477	HS 5576 B	C 789	33	4.3	774	5	BU316793	603855209
C 716	33.2	4.3	791	4	BI105506	602891839	C 790	33	4.3	788	6	CD906120	G468.103P
C 717	33.2	4.3	795	4	BG889180	EST515031	C 791	33	4.3	790	9	CL554281	OB_Ba000
C 718	33.2	4.3	803	5	BU233923	603411828	C 792	33	4.3	795	8	BZ428278	BONNM31TR
C 719	33.2	4.3	809	9	CG962465	MBENH21TF	C 793	33	4.3	811	7	CN227619	RJB021F04
C 720	33.2	4.3	817	4	BM410777	EST585104	C 794	33	4.3	814	8	BZ110323	CH230-230
C 721	33.2	4.3	894	7	CK796769	AGENCOURT	C 795	33	4.3	820	9	CNS0230Z	Tetraodon
C 722	33.2	4.3	903	9	CNS06X04	AL419114 T7 end of	C 796	33	4.3	821	8	BH678554	BOHYJ16TR
C 723	33.2	4.3	920	7	CK363090	CK263090 EST709168	C 797	33	4.3	832	7	CO580772	ILLUMIGEN
C 724	33.2	4.3	956	5	BQ945685	BQ945685 AGENCOURT	C 798	33	4.3	839	8	BZ519182	BZ519182 BOMRG78TR
C 725	33.2	4.3	1115	8	CC300704	CH261-68L	C 799	33	4.3	846	9	CL839176	OR_CBa006
C 726	33.2	4.3	1319	9	CG745602	CG745602 P038-3-C1	C 800	33	4.3	865	9	CR258613	Reverse s
C 727	33	4.3	173	9	CL002188	CL002188 02S0069-0	C 801	33	4.3	875	9	CN329377	AGENCOURT
C 728	33	4.3	232	5	BQ156654	BQ156654 NF095B081	C 802	33	4.3	900	4	BI654649	603285564
C 729	33	4.3	240	2	BB107987	BB107987 BB107987	C 803	33	4.3	913	6	CB229507	AGENCOURT
C 730	33	4.3	249	1	AI864971	AI864971 wk06D03.x	C 804	33	4.3	913	9	CNS0611Q	T7 end of
C 731	33	4.3	295	5	BU618324	BU618324 UI-H-FH1-	C 805	33	4.3	923	8	BH146438	ENTPR40TF
C 732	33	4.3	418	1	AV788577	AV788577 AV788577	C 806	33	4.3	966	2	BF302958	602030858
C 733	33	4.3	427	8	BZ768512	BZ768512 SALK_1403	C 807	33	4.3	977	4	BI559237	603240863
C 734	33	4.3	434	1	AI752199	AI752199 cn14C06.Y	C 808	33	4.3	1029	1	AL573715	AL573715
C 735	33	4.3	462	8	BH706749	BH706749 BOMDH80TR	C 809	33	4.3	1071	9	CNS057KE	Tetraodon
C 736	33	4.3	480	8	BH440195	BH440195 BOGIN57TF	C 810	33	4.3	1117	8	CC216496	CH261-781
C 737	33	4.3	490	7	CN551520	CN551520 tad73h06.	C 811	33	4.3	1200	9	CNS016CI	AL106572
C 738	33	4.3	494	2	BF546023	BF546023 UI-R-C2p-	C 812	33	4.3	1212	8	BZ691036	Drosophil
C 739	33	4.3	495	2	AW410218	AW410218 fh05c12.Y	C 813	33	4.3	1389	9	CG751034	SP_Ba000
C 740	33	4.3	508	7	CO644267	CO644267 USDA-FP_1	C 814	33	4.3	1871	3	CNS0A2XR	Arabidops
C 741	33	4.3	511	7	CN558588	N37165 18375 Lambd	C 815	33	4.3	2001	3	BC015705	Homo sapi
C 742	33	4.3	511	7	N37165	CE022124 tigr-gss-	C 816	33	4.3	213	7	CF371656	CSECS015E
C 743	33	4.3	518	9	CE022124	BU895718 x030A07 P	C 817	32.8	4.3	244	1	AV360468	AV360468
C 744	33	4.3	521	5	BU895718	BI770986 603055323	C 818	32.8	4.3	245	1	AV315185	AV315185
C 745	33	4.3	522	8	B83744	B83744 CpG0094A Cp	C 819	32.8	4.3	249	2	BB074609	BB074609
C 746	33	4.3	524	4	BI770986	BQ002597 UI-H-B11-	C 820	32.8	4.3	249	2	BB141111	BB141111
C 747	33	4.3	525	5	BQ002597	AL914516 AL914516	C 821	32.8	4.3	254	7	CF969459	lag68a09.
C 748	33	4.3	539	1	AL914516	BU696710 LL2in1083	C 822	32.8	4.3	257	7	CF379612	lad06d07.
C 749	33	4.3	540	8	AQ680994	AQ680994 HS_5492 B	C 823	32.8	4.3	258	1	AV255530	AV255530
C 750	33	4.3	540	8	AQ680994	CF949646 UI-M-HK0-	C 824	32.8	4.3	280	1	AV052841	AV052841
C 751	33	4.3	548	7	CF949646	CL554363 OB_Ba000	C 825	32.8	4.3	280	2	BB432211	BB432211
C 752	33	4.3	558	9	CL554363	BZ904403 CH240_25P	C 826	32.8	4.3	285	7	CK372120	lai33h10.
C 753	33	4.3	568	8	BZ904403	BM669984 UI-E-DW1-	C 827	32.8	4.3				
C 754	33	4.3	576	4	BM669984								

C 828	32.8	4.3	294	2	BB026976	BB026976	BB026976	901	32.8	4.3	896	9	CG929597	CG929597	MBEJP65TF
C 829	32.8	4.3	298	2	BB110605	BB110605	BB110605	902	32.8	4.3	898	9	CG166446	CG166446	PUFQN92TB
C 830	32.8	4.3	299	2	BB124772	BB124772	BB124772	C 903	32.8	4.3	911	9	CNS070R2	AL423972	T7 end of
C 831	32.8	4.3	303	2	BB221261	BB221261	BB221261	C 904	32.8	4.3	914	8	AZ545365	AZ545365	ENTFP91TF
C 832	32.8	4.3	314	2	BB719396	BB719396	BB719396	905	32.8	4.3	915	9	CNS02K1P	AL201552	Tetraodon
C 833	32.8	4.3	320	2	BB338492	BB338492	BB338492	906	32.8	4.3	931	8	BH135538	BH135538	ENTOS03TF
C 834	32.8	4.3	337	2	BB125831	BB125831	BB125831	907	32.8	4.3	942	9	CNS06NCW	AL406614	T7 end of
C 835	32.8	4.3	346	4	BG406288	sac29h02.	BG406288	C 908	32.8	4.3	998	9	CL070481	CL070481	CH216-118
C 836	32.8	4.3	348	4	BG092709	mac15h11.	BG092709	909	32.8	4.3	1101	9	CNS016QS	AL107086	Drosoph11
C 837	32.8	4.3	357	2	BB745689	BB745689	BB745689	910	32.8	4.3	1200	8	CC297017	CC297017	CH261-43H
C 838	32.8	4.3	373	1	AL385382	MTBC28C06	AL385382	911	32.8	4.3	1214	9	AG340923	AG340923	Mus muscu
C 839	32.8	4.3	380	7	CF424488	lad31d05.	CF424488	C 912	32.8	4.3	1219	9	CL033692	CL033692	CH216-36N
C 840	32.8	4.3	381	6	CA890445	B0159D04-	CA890445	913	32.8	4.3	1606	3	BC068017	BC068017	Homo sapi
C 841	32.8	4.3	382	1	AL385383	MTBC28C06	AL385383	C 914	32.8	4.3	2148	3	AK035990	AK035990	Mus muscu
C 842	32.8	4.3	386	6	CD706108	EST22635	CD706108	C 915	32.6	4.3	225	4	BI691815	BI691815	603307537
C 843	32.8	4.3	408	2	BF561593	UI-R-C0-i	BF561593	916	32.6	4.3	241	8	BZ523111	BZ523111	BOKAD78TR
C 844	32.8	4.3	414	1	AA710655	vt43e10.r	AA710655	917	32.6	4.3	261	4	BI038664	BI038664	IL3-NT028
C 845	32.8	4.3	414	2	BF387419	UI-R-CA1-	BF387419	918	32.6	4.3	261	4	BI039792	BI039792	IL3-NT028
C 846	32.8	4.3	426	2	AW013852	UI-H-B10-	AW013852	C 919	32.6	4.3	269	2	BE240137	BE240137	EST404186
C 847	32.8	4.3	448	8	AQ870616	nbeb0040E	AQ870616	C 920	32.6	4.3	303	1	AI805603	AI805603	tx97d08.x
C 848	32.8	4.3	452	2	BB776148	BB776148	BB776148	921	32.6	4.3	351	6	CB780941	CB780941	AMGNNUC:M
C 849	32.8	4.3	512	7	CF745811	UI-M-GV0-	CF745811	C 922	32.6	4.3	433	1	AL675598	AL675598	AL675598
C 850	32.8	4.3	518	5	BQ554425	H4028A11-	BQ554425	923	32.6	4.3	441	5	BQ321431	BQ321431	MR3-CT046
C 851	32.8	4.3	522	2	BB751730	BB751730	BB751730	C 924	32.6	4.3	481	2	BE251135	BE251135	601107196
C 852	32.8	4.3	541	7	CN681524	E0151F11-	CN681524	C 925	32.6	4.3	488	8	BH041279	BH041279	RPCI-24-3
C 853	32.8	4.3	541	7	CN686589	E0227D11-	CN686589	926	32.6	4.3	517	8	AQ510066	AQ510066	nbxb0094B
C 854	32.8	4.3	562	9	CL764258	OR_BBa013	CL764258	927	32.6	4.3	528	9	CE819937	CE819937	tigr-gs8-
C 855	32.8	4.3	563	5	BQ398706	NISC_m010	BQ398706	C 928	32.6	4.3	538	5	BQ198195	BQ198195	NXLV126_H
C 856	32.8	4.3	572	2	BF358706	PH1-ET000	BF358706	C 929	32.6	4.3	544	8	AQ983337	AQ983337	RPCI-23-3
C 857	32.8	4.3	576	7	CF430166	PH1_26_H0	CF430166	C 930	32.6	4.3	555	8	BZ277916	BZ277916	CH230-356
C 858	32.8	4.3	577	6	CB442355	692932_MA	CB442355	931	32.6	4.3	558	8	B93214	B93214	CIT-HSP-217
C 859	32.8	4.3	587	6	CD153781	ML1-0035T	CD153781	C 932	32.6	4.3	566	5	BP764509	BP764509	BP764509
C 860	32.8	4.3	593	7	CN675335	A0962A07-	CN675335	C 933	32.6	4.3	574	4	BG161828	BG161828	df69a06.x
C 861	32.8	4.3	605	8	AZ092149	RPCI-23-4	AZ092149	C 934	32.6	4.3	578	1	AL722362	AL722362	AL722362
C 862	32.8	4.3	609	9	CL606970	CH240_170	CL606970	C 935	32.6	4.3	585	8	AZ320089	AZ320089	1M0039P20
C 863	32.8	4.3	610	1	AI788741	UK53d08.x	AI788741	936	32.6	4.3	590	7	CK089573	CK089573	C019P10.3
C 864	32.8	4.3	612	7	CF891779	A0100H11-	CF891779	937	32.6	4.3	594	8	BH769474	BH769474	BMBAC366A
C 865	32.8	4.3	612	9	CL712399	OR_BBa003	CL712399	C 938	32.6	4.3	595	8	BH869671	BH869671	hl46605.b
C 866	32.8	4.3	614	8	BH760525	BMBAC313F	BH760525	C 939	32.6	4.3	600	7	CO372163	CO372163	tah98a06.
C 867	32.8	4.3	621	4	BJ711905	BJ711905	BJ711905	C 940	32.6	4.3	630	1	AT003850	AT003850	AT003850
C 868	32.8	4.3	633	5	BM991828	UI-H-DP1-	BM991828	C 941	32.6	4.3	650	2	BE427659	BE427659	PSR7312_I
C 869	32.8	4.3	635	4	BG443516	GA_Ea002	BG443516	C 942	32.6	4.3	658	2	AW684747	AW684747	NF021F05N
C 870	32.8	4.3	636	2	AW586848	EST318471	AW586848	C 943	32.6	4.3	688	7	CO176656	CO176656	NDL1_63_H
C 871	32.8	4.3	639	4	BJ264614	BJ264614	BJ264614	944	32.6	4.3	724	7	CN041380	CN041380	nm_40h_g5
C 872	32.8	4.3	642	7	CK315060	SB02041A2	CK315060	C 945	32.6	4.3	724	8	BZ722129	BZ722129	PUDAN39TD
C 873	32.8	4.3	660	9	CL757894	OR_BBa012	CL757894	C 946	32.6	4.3	727	4	BG723382	BG723382	602694045
C 874	32.8	4.3	665	8	AQ878469	HS_3081_A	AQ878469	C 947	32.6	4.3	729	7	CN531184	CN531184	UI-M-H00-
C 875	32.8	4.3	665	9	BX189742	Danio rer	BX189742	C 948	32.6	4.3	740	1	AJ446279	AJ446279	AJ446279
C 876	32.8	4.3	678	7	CO682600	DG11-156f	CO682600	C 949	32.6	4.3	746	5	BU121925	BU121925	603146640
C 877	32.8	4.3	680	2	BB127711	BB127711	BB127711	C 950	32.6	4.3	746	9	CG252503	CG252503	OG1AR66TV
C 878	32.8	4.3	685	8	AQ322944	RPCI11-10	AQ322944	951	32.6	4.3	751	9	CR121431	CR121431	Reverse8_B
C 879	32.8	4.3	686	5	BX112698	BX112698	BX112698	952	32.6	4.3	751	9	CG252492	CG252492	OG1AR66TH
C 880	32.8	4.3	693	4	BI503838	BB170026B	BI503838	C 953	32.6	4.3	758	5	BU225465	BU225465	603398746
C 881	32.8	4.3	694	9	CL819689	OR_CBa003	CL819689	C 954	32.6	4.3	767	5	BP433918	BP433918	BP433918
C 882	32.8	4.3	706	4	BJ282350	BJ282350	BJ282350	C 955	32.6	4.3	769	7	CO176746	CO176746	NDL1_63_H
C 883	32.8	4.3	717	9	CL596203	OB_Ba005	CL596203	956	32.6	4.3	775	2	BE620997	BE620997	601493580
C 884	32.8	4.3	723	8	BH521966	BOGEI27TF	BH521966	957	32.6	4.3	780	4	BI251779	BI251779	602994285
C 885	32.8	4.3	727	8	BH035130	RPCI-24-3	BH035130	C 958	32.6	4.3	780	8	AQ349389	AQ349389	RPCI11-11
C 886	32.8	4.3	728	7	CK303096	SB02017A2	CK303096	959	32.6	4.3	790	5	BU207869	BU207869	603950035
C 887	32.8	4.3	730	8	AQ243297	HS_2060_B	AQ243297	960	32.6	4.3	796	4	BG780413	BG780413	SEAUMC000
C 888	32.8	4.3	741	8	BZ718947	PUCFY59TD	BZ718947	C 961	32.6	4.3	796	5	BP435042	BP435042	BP435042
C 889	32.8	4.3	747	8	BZ119136	CC746447	BZ119136	962	32.6	4.3	810	8	BZ970980	BZ970980	PUGEA18TB
C 890	32.8	4.3	765	9	CC746447	BJ726391	CC746447	963	32.6	4.3	823	9	CG673724	CG673724	trb1456_t
C 891	32.8	4.3	768	4	BJ726391	BJ726391	BJ726391	964	32.6	4.3	834	4	BG540058	BG540058	602568689
C 892	32.8	4.3	803	9	CC738931	ZMMBBb010	CC738931	C 965	32.6	4.3	844	8	AZ687551	AZ687551	ENTL253TR
C 893	32.8	4.3	808	9	BX196960	Danio rer	BX196960	966	32.6	4.3	847	9	CG947697	CG947697	MBEDW26TF
C 894	32.8	4.3	821	9	CNS009LA	Drosoph11	AL053819	967	32.6	4.3	871	9	CG173767	CG173767	PUFVI66TD
C 895	32.8	4.3	865	6	CA106362	SCQGRH101	CA106362	968	32.6	4.3	872	9	CG328446	CG328446	OG1CB08TH
C 896	32.8	4.3	867	7	CK153073	FGAS03162	CK153073	969	32.6	4.3	880	8	AQ750737	AQ750737	HS_5574_B
C 897	32.8	4.3	869	4	BG754409	602710024	BG754409	C 970	32.6	4.3	895	9	CNS06WAS	AL418202	T3_end_of
C 898	32.8	4.3	869	7	CF618170	AGENCOURT	CF618170	C 971	32.6	4.3	897	5	BU142210	BU142210	603135333
C 899	32.8	4.3	872	7	CN756996	ID0AAA1AE	CN756996	972	32.6	4.3	919	8	BZ722126	BZ722126	PUDAN39TB
C 900	32.8	4.3	891	8	AZ541750	ENTEN79TF	AZ541750	C 973	32.6	4.3	920	7	CK417925	CK417925	AUF_ipInt

C 974 32.6 4.3 922 8 AQ901220
C 975 32.6 4.3 931 1 AL580292
C 976 32.6 4.3 931 8 AZ672194 ENTH57TF
977 32.6 4.3 931 9 CNS0378W
978 32.6 4.3 946 9 CG130069
979 32.6 4.3 954 7 CO758627 brain_EST
980 32.6 4.3 967 9 CL018559 CH216-3L1
C 981 32.6 4.3 997 9 CG130068
C 982 32.6 4.3 998 9 CL125118
C 983 32.6 4.3 1009 9 CNS0601A
C 984 32.6 4.3 1032 9 CNS006YP
C 985 32.6 4.3 1075 2 BE781356
C 986 32.6 4.3 1089 9 CNS051RV
C 987 32.6 4.3 1095 8 CC290569
C 988 32.6 4.3 1125 3 CR677068
C 989 32.4 4.2 1197 2 BE319519
C 990 32.4 4.2 201 2 BE320839
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C 993 32.4 4.2 288 2 BB486727
994 32.4 4.2 292 2 BB078719
C 995 32.4 4.2 305 2 BB201683
C 996 32.4 4.2 307 2 AW881332
C 997 32.4 4.2 341 5 BY220133
C 998 32.4 4.2 352 5 BY220208
C 999 32.4 4.2 379 5 BU867490
C1000 32.4 4.2 391 1 AA588507
C1001 32.4 4.2 393 1 AI974086
1002 32.4 4.2 398 1 AU032743
C1003 32.4 4.2 402 2 BE825092
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C1009 32.4 4.2 446 9 CR049015
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C1012 32.4 4.2 477 7 CN058883
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1015 32.4 4.2 493 7 CN818094
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C1031 32.4 4.2 611 8 AZ426862
C1032 32.4 4.2 623 6 CD341634
1033 32.4 4.2 624 8 AZ271952
C1034 32.4 4.2 630 7 CK654582
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C1037 32.4 4.2 635 6 CD322136
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4.2 32.2 C1119

BJ023215 BJ023215
CL566362 OB_Ba003
BU368687 603595693
BX782077 BX782077
CN590843 TTE000119
BU212422 604157440
BU802995 SJFAPH09
CR2229846 Reverse s
BZ3957777 EINBN44TR
CC835606 ZMMBBb018
AL406305 T3 end of
AG486476 Mus muscu
CR243525 Forward s
CL813059 OR_CBa002
BU393380 603801243
AG303296 Mus muscu
CN324769 AGENCOURT
AG317067 Mus muscu
BH932802 ode98h01.
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AZ669779 ENTIQ53TR
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CC588285 CH240_386
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CG962271 MBELJ64TR
AL208607 Tetraodon
CB203539 AGENCOURT
BX968158 Forward s
CL101062 ISB1_-3601
AL439804 T7 end of
CL112104 ISB1_-56G2
AL412447 T3 end of
AL062483 Drosophil
CC191358 CH261-40L
CC291618 CH261-61D
CG755657 P051-1-G1
CC232487 CH261-183
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CK398902 AGENCOURT
BX489946 DKFPZp686I
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CF228104 PtaXM0008
BE237502 146821_MA
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CB105148 K-EST0103
CR480030 Medicago
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AI446875 EpMS060_E
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BZ904289 CH240_25H
AQ023353 HS_2179_B
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BE645262 7e67b12.x
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AV712380 AV712380
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AL819085 AL819085
AW183555 xj75h12.x
CG925126 MBFL61TR
BE458935 EST414227
BE360184 DG1_61_A1

1120	32.2	4.2	483	7	H59583	H59583 yr29f12.r1	1193	32.2	4.2	799	9	CR230522	Reverse s
c1121	32.2	4.2	495	5	BX480191	BX480191 DKF2p686G	c1194	32.2	4.2	802	9	CG966993	MBECN41TF
1122	32.2	4.2	496	2	BF574405	BF574405 602131617	c1195	32.2	4.2	805	5	BW135784	BW135784
c1123	32.2	4.2	497	7	CK512626	CK512626 rswd0_01	1196	32.2	4.2	807	2	BF028817	BF028817 601764778
1124	32.2	4.2	502	2	BE424118	BE424118 WHE0076_F	c1197	32.2	4.2	812	6	CB678341	CB678341 OSJNE16C
1125	32.2	4.2	502	8	AZ440820	AZ440820 1M0232001	c1198	32.2	4.2	819	9	BX972981	Reverse s
c1126	32.2	4.2	504	4	BG946992	BG946992 IPI_2_C03	1199	32.2	4.2	828	9	CC517171	CH240_363
c1127	32.2	4.2	505	4	BG946993	BG946993 IPI_2_C04	1200	32.2	4.2	831	5	BU382156	603860486
c1128	32.2	4.2	506	8	AQ767932	AQ767932 HS_3089_A	1201	32.2	4.2	837	7	CK305054	SB02027A2
1129	32.2	4.2	516	6	CB678798	CB678798 OSJNEf01H	1202	32.2	4.2	842	5	BU307860	603539737
1130	32.2	4.2	523	2	AW828046	AW828046 rac1a02_Y	1203	32.2	4.2	867	5	BU794491	SJF2CWA06
1131	32.2	4.2	523	2	BE879702	BE879702 601491796	c1204	32.2	4.2	886	8	BH147852	ENTQB64TF
1132	32.2	4.2	523	8	AQ833770	AQ833770 HS_5315_A	c1205	32.2	4.2	896	9	CNS032XQ	Tetraodon
1133	32.2	4.2	529	5	BX768632	BX768632 BX768632	c1206	32.2	4.2	899	9	CG959519	MBEKJ26TR
1134	32.2	4.2	530	5	BQ596395	BQ596395 PFESToab3	c1207	32.2	4.2	902	8	AZ677735	ENTLE14TF
1135	32.2	4.2	539	1	AI652367	AI652367 wb60g02.X	c1208	32.2	4.2	911	9	CC547509	CH240_430
1136	32.2	4.2	539	6	CD734523	CD734523 4048666_1	c1209	32.2	4.2	918	9	CG958349	MBEHT76TR
c1137	32.2	4.2	541	5	BU801309	BU801309 SJF2DBH01	1210	32.2	4.2	919	9	CNS006NC	Drosophil
c1138	32.2	4.2	545	5	BU779820	BU779820 SJFQF05	1211	32.2	4.2	931	5	BU152317	AGENCOURT
1139	32.2	4.2	557	4	BG457346	BG457346 NF103F03P	c1212	32.2	4.2	941	5	BU795265	SJF2DMF04
1140	32.2	4.2	567	8	BH328105	BH328105 CH230-45P	1213	32.2	4.2	953	9	CL792483	OR_CBa000
c1141	32.2	4.2	567	9	CR495928	CR495928 Medicago	1214	32.2	4.2	985	3	CR719563	Tetraodon
1142	32.2	4.2	569	9	FR0025736	AL018572 F_rubripe	c1215	32.2	4.2	1004	4	BG244503	602356158
c1143	32.2	4.2	585	1	AI795367	AI795367 605011H02	c1216	32.2	4.2	1023	5	BX355747	BX355747
c1144	32.2	4.2	585	7	CN127931	CN127931 RH0H1_26_	1217	32.2	4.2	1025	5	BQ676015	AGENCOURT
1145	32.2	4.2	588	4	BJ040890	BJ040890 BJ040890_	1218	32.2	4.2	1038	7	CK205364	FGA501683
c1146	32.2	4.2	594	4	BJ303164	BJ303164 BJ303164	1219	32.2	4.2	1043	4	BG482491	602527271
1147	32.2	4.2	600	4	BJ287188	BJ287188 BJ287188	1220	32.2	4.2	1054	8	CC257049	CH261-42C
1148	32.2	4.2	600	5	BQ539390	BQ539390 MEST615-D	c1221	32.2	4.2	1080	9	CNS008PP	AL069494 Drosophil
c1149	32.2	4.2	606	7	CN140305	CR140305 OX1_35_G1	1222	32.2	4.2	1093	9	CNS05760	AL324249 Tetraodon
c1150	32.2	4.2	607	9	CR498679	CR498679 Medicago	1223	32.2	4.2	1114	1	AL541168	AL541168
1151	32.2	4.2	613	8	AZ898966	AZ898966 RPCI-24-2	c1224	32.2	4.2	1132	5	BX402111	BX402111
c1152	32.2	4.2	617	5	BQ635428	BQ635428 1091070D0	1225	32.2	4.2	1540	3	CR620910	full-leng
1153	32.2	4.2	619	8	BH300262	BH300262 CH230-109	1226	32.2	4.2	1731	3	CR604240	full-leng
c1154	32.2	4.2	621	9	CC740710	CC740710 ZMWBBb010	1227	32.2	4.2	3141	3	BC030234	Homo sapi
1155	32.2	4.2	623	8	AQ471143	AQ471143 CITBI-E1-	1228	32.2	4.2	5656	3	BSM803132	AL831819 Homo sapi
c1156	32.2	4.2	626	2	BE922735	BE922735 EST426504	1229	32	4.2	242	6	CB974776	CB974776 CAB30005_
c1157	32.2	4.2	637	5	BQ172575	BQ172575 1091024E0	c1230	32	4.2	274	5	BP507583	BP507583
c1158	32.2	4.2	638	6	CF181319	CF181319 818131_MA	c1231	32	4.2	280	2	BE664456	BE664456 148931_MA
1159	32.2	4.2	639	5	BP166240	BP166240 BP166240	c1232	32	4.2	282	5	BP634093	BP634093
1160	32.2	4.2	639	6	CB874431	CB874431 HX05D24w	c1233	32	4.2	314	1	AV239254	AV239254
1161	32.2	4.2	641	3	CR653070	CR653070 Tetraodon	c1234	32	4.2	315	2	BF388003	BF388003
1162	32.2	4.2	646	7	CF925320	CF925320 M1_MQ1_07	1235	32	4.2	320	4	BM435669	BM435669 1Ru8D1.ab
1163	32.2	4.2	647	5	BW266341	BW266341 BW266341	c1236	32	4.2	329	9	CR404678	Arabidops
1164	32.2	4.2	650	7	CF925265	CF925265 M1_MQ1_07	c1237	32	4.2	336	9	CR401373	Arabidops
c1165	32.2	4.2	656	8	AQ060140	AQ060140 CIT-HSP-2	c1238	32	4.2	338	6	CD139772	MGI-0064T
1166	32.2	4.2	657	7	CO618528	CO618528 DG9-18791	1239	32	4.2	359	4	BG407791	dab23d11.
c1167	32.2	4.2	658	7	CF517560	CF517560 CAP0005_I	c1240	32	4.2	378	9	CR311593	Medicago
c1168	32.2	4.2	661	7	CF397053	CF397053 RTDS2_26_	c1241	32	4.2	394	1	AI432065	AI432065 th34902.X
c1169	32.2	4.2	662	4	BJ303178	BJ303178 BJ303178_	1242	32	4.2	401	5	BY577961	BY577961
c1170	32.2	4.2	662	7	CK488081	CK488081 rswab0_00	c1243	32	4.2	406	9	BX156914	BX156914
c1171	32.2	4.2	669	9	CL158220	CL158220 104_346_1	1244	32	4.2	407	8	AQ027483	AQ027483
1172	32.2	4.2	676	5	BU281579	BU281579 603600889	c1245	32	4.2	414	7	N73351	N73351 YV72B10.r1
c1173	32.2	4.2	680	7	CK210385	CK210385 FGAS02219	c1246	32	4.2	422	9	BX184294	BX184294
1174	32.2	4.2	686	9	BX176061	BX176061 Danio rer	c1247	32	4.2	453	2	BF961662	BF961662
1175	32.2	4.2	689	4	BJ539158	BJ539158 BJ539158	1248	32	4.2	461	2	AW406219	AW406219
1176	32.2	4.2	695	7	CF925058	CF925058 M1_MQ1_02	c1249	32	4.2	472	2	BE107749	BE107749
1177	32.2	4.2	697	4	BJ310185	BJ310185 BJ310185	c1250	32	4.2	475	8	CC456900	SALK_1013
c1178	32.2	4.2	700	2	BE796759	BE796759 601587384	1251	32	4.2	485	8	BZ515704	BZ515704 BOMRK53TR
1179	32.2	4.2	705	4	BJ309035	BJ309035 BJ309035	c1252	32	4.2	488	2	BE119869	BE119869
c1180	32.2	4.2	709	7	CN134434	CN134434 OX1_26_G1	c1253	32	4.2	490	8	B37654	B37654 HS-1044-B1-
1181	32.2	4.2	722	9	CE379425	CE379425 tigr-gss-	c1254	32	4.2	496	9	BX127555	BX127555
1182	32.2	4.2	727	8	BZ022058	BZ022058 oee39g02.	c1255	32	4.2	505	8	BZ116059	BZ116059
c1183	32.2	4.2	730	8	BH015255	BH015255 TDGBW82TH	c1256	32	4.2	513	6	CA240585	SCSFL406
c1184	32.2	4.2	731	5	BW158254	BW158254 BW158254	c1257	32	4.2	515	5	BM991659	BM991659
c1185	32.2	4.2	734	7	CK769563	CK769563 957607_MA	1258	32	4.2	517	8	AQ467042	AQ467042 HS_5192_B
1186	32.2	4.2	740	9	AG451803	AG451803 Mus muscu	c1259	32	4.2	518	6	CA602894	wrl.pk000
1187	32.2	4.2	742	5	BU686763	BU686763 UI-CF-DU1	1260	32	4.2	535	9	CR104702	CR104702
c1188	32.2	4.2	756	7	CR426111	CR426111 CR426111	c1261	32	4.2	536	2	BE593965	BE593965
c1189	32.2	4.2	761	8	BZ856818	BZ856818 CH240_206	c1262	32	4.2	536	4	BI799552	BI799552
c1190	32.2	4.2	762	5	BU718974	BU718974 SJM2CPC11	1263	32	4.2	538	1	AV757416	AV757416
1191	32.2	4.2	772	5	BU140867	BU140867 603008177	c1264	32	4.2	545	7	CN548536	EST_16174
c1192	32.2	4.2	791	8	BZ391790	BZ391790 EINBW37TF	1265	32	4.2	549	9	CE506899	tigr-gss-

1266	32	4.2	553	8	AZ722165	AZ722165	RPCI-24-6	1339	32	4.2	863	9	CG970824	CG970824	MBEDS06TR
1267	32	4.2	559	4	BI290756	BI290756	UI-R-DK0-	1340	32	4.2	874	9	CR228736	CR228736	Forward s
1268	32	4.2	560	2	BF952030	BF952030	QV2-NN004	1341	32	4.2	874	9	CG064557	CG064557	FUJCK03TD
1269	32	4.2	562	7	CK824515	CK824515	ig27e03.y	1342	32	4.2	877	5	BU905384	BU905384	AGENCOURT
1270	32	4.2	566	1	AL594449	AL594449	AL594449	1343	32	4.2	877	9	CG147800	CG147800	PUIHG69TD
1271	32	4.2	567	4	BJ046697	BJ046697	BJ046697	1344	32	4.2	896	8	AZ687152	AZ687152	ENTIX91TF
1272	32	4.2	568	5	BJ335744	BJ335744	BJ335744	1345	32	4.2	924	9	CG088272	CG088272	FUJBR35TB
1273	32	4.2	575	9	CE348425	CE348425	tigr-gss-	1346	32	4.2	925	5	BU903869	BU903869	AGENCOURT
1274	32	4.2	586	5	BP027873	BP027873	BP027873	1347	32	4.2	933	4	BI410497	BI410497	602963187
1275	32	4.2	593	2	BE390303	BE390303	601286103	1348	32	4.2	941	5	BU292092	BU292092	603607570
1276	32	4.2	594	8	BZ220995	BZ220995	CH230-467	1349	32	4.2	1001	8	AZ687340	AZ687340	ENTKS07TR
1277	32	4.2	595	4	BI380977	BI380977	BFLG1_002	1350	32	4.2	1011	9	CNS050BR	CNS050BR	Tetraodon
1278	32	4.2	595	9	CE205854	CE205854	tigr-gss-	1351	32	4.2	1017	4	BM560805	BM560805	AGENCOURT
1279	32	4.2	600	8	BH441730	BH441730	BOHKB25TR	1352	32	4.2	1025	9	CNS00AIZ	CNS00AIZ	Drosophil
1280	32	4.2	601	8	BZ082860	BZ082860	11G84a01.	1353	32	4.2	1027	5	BU134262	BU134262	603121030
1281	32	4.2	603	6	CA727822	CA727822	wdilc.pk0	1354	32	4.2	1035	9	CNS00ZD5	CNS00ZD5	Drosophil
1282	32	4.2	607	8	AQ760107	AQ760107	HS_2181_A	1355	32	4.2	1087	8	CC231266	CC231266	CH261-32P
1283	32	4.2	611	6	CF213213	CF213213	CGF100063	1356	32	4.2	1101	9	CNS00LO0	CNS00LO0	Drosophil
1284	32	4.2	614	6	CA755071	CA755071	BR0300120	1357	32	4.2	1126	8	CC216546	CC216546	CH261-78J
1285	32	4.2	628	9	CR239534	CR239534	Forward s	1358	32	4.2	1189	6	CB588920	CB588920	AGENCOURT
1286	32	4.2	633	9	CR314109	CR314109	Medicago	1359	32	4.2	1251	6	CD495791	CD495791	CDA18-F04
1287	32	4.2	634	9	CL637973	CL637973	CH243-9G2	1360	32	4.2	1284	9	AG333588	AG333588	Mus muscu
1288	32	4.2	635	5	BU989807	BU989807	HF22M02r	1361	32	4.2	1397	4	BG751380	BG751380	602730136
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1290	32	4.2	646	6	CB176139	CB176139	pl18d11.y	1363	32	4.2	2244	3	CR699138	CR699138	Tetraodon
1291	32	4.2	650	5	BU996723	BU996723	HMI4116r	1364	31.8	4.2	177	1	AI505294	AI505294	vq76h12.x
1292	32	4.2	654	5	BU996533	BU996533	HMI3017r	1365	31.8	4.2	199	4	BI966282	BI966282	id50d03.x
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1295	32	4.2	665	9	CR152699	CR152699	Reverse s	1368	31.8	4.2	278	7	CN585563	CN585563	USDA-FP_1
1296	32	4.2	666	5	BW302935	BW302935	BW302935	1369	31.8	4.2	294	2	AW951272	AW951272	EST363342
1297	32	4.2	669	6	CB338971	CB338971	pl37b07.y	1370	31.8	4.2	331	7	CR460477	CR460477	CR460477
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1299	32	4.2	671	5	BW370395	BW370395	BW370395	1372	31.8	4.2	346	2	BE102793	BE102793	UI-R-BT1-
1300	32	4.2	674	2	BE365933	BE365933	PI1_2_C03	1373	31.8	4.2	352	1	AA848610	AA848610	EST191370
1301	32	4.2	678	5	BW189805	BW189805	BW189805	1374	31.8	4.2	356	7	CK320290	CK320290	L3P02a02
1302	32	4.2	684	5	BW189735	BW189735	BW189735	1375	31.8	4.2	363	8	AQ205644	AQ205644	HS_3235_B
1303	32	4.2	685	5	BW984227	BW984227	UI-CF-EC1	1376	31.8	4.2	378	2	BE926172	BE926172	PMI-BN017
1304	32	4.2	692	5	BW299580	BW299580	BW299580	1377	31.8	4.2	381	8	AZ357676	AZ357676	1M0099L21
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1306	32	4.2	701	6	CA504839	CA504839	UI-R-FJ0-	1379	31.8	4.2	387	6	CB434520	CB434520	611142_MA
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1308	32	4.2	705	4	BG845276	BG845276	1024009E1	1381	31.8	4.2	402	4	BM432565	BM432565	1JEJ11C10
1309	32	4.2	707	9	CR145607	CR145607	Forward s	1382	31.8	4.2	404	6	CF134418	CF134418	CFG11-82.
1310	32	4.2	708	9	EX127358	EX127358	Danio rer	1383	31.8	4.2	404	6	CG604911	CG604911	WHE0944_H
1311	32	4.2	710	5	BW485785	BW485785	BW485785	1384	31.8	4.2	407	4	BG604911	BG604911	om98a02_s
1312	32	4.2	711	5	BW686404	BW686404	UI-CF-DU1	1385	31.8	4.2	410	1	AA931390	AA931390	om98a02_s
1313	32	4.2	714	9	CC921944	CC921944	t060113ba	1386	31.8	4.2	417	1	AA460165	AA460165	zx60g12.s
1314	32	4.2	729	5	BU282051	BU282051	603867170	1387	31.8	4.2	425	8	AQ210977	AQ210977	HS_3237_A
1315	32	4.2	736	8	CC074345	CC074345	CSU-K33r.	1388	31.8	4.2	436	1	AA670540	AA670540	v102e09.r
1316	32	4.2	739	9	CC519277	CC519277	CH240_366	1389	31.8	4.2	441	8	BH777145	BH777145	fzmb013f0
1317	32	4.2	754	4	BF982545	BF982545	602308154	1390	31.8	4.2	444	1	AI248625	AI248625	qh77b11.x
1318	32	4.2	755	8	BZ462323	BZ462323	BO0AA76TF	1391	31.8	4.2	448	7	CF803224	CF803224	rd95g04.y
1319	32	4.2	757	4	BJ569800	BJ569800	BJ569800	1392	31.8	4.2	453	2	AW138892	AW138892	UI-H-BI1-
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1329	32	4.2	791	7	CN173332	CN173332	AGENCOURT	1402	31.8	4.2	489	7	CN590229	CN590229	TTE000009
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1331	32	4.2	821	2	BE548097	BE548097	601072338	1404	31.8	4.2	506	6	C97602	C97602	C97602_Rice
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1333	32	4.2	826	9	BX200514	BX200514	Danio rer	1406	31.8	4.2	516	7	CF529795	CF529795	UI-1-BC1p
1334	32	4.2	838	7	CO398600	CO398600	AGENCOURT	1407	31.8	4.2	517	5	BQ090146	BQ090146	rc62b04.y
1335	32	4.2	841	7	CK775121	CK775121	963935_MA	1408	31.8	4.2	519	2	BE429479	BE429479	TAS000.E1
1336	32	4.2	847	6	CB559180	CB559180	AGENCOURT	1409	31.8	4.2	534	6	CD534966	CD534966	54L6_Arab
1337	32	4.2	848	7	CK804972	CK804972	AGENCOURT	1410	31.8	4.2	535	8	AQ536694	AQ536694	RPCI-11-3
1338	32	4.2	857	7	CN227732	CN227732	RJB094F05	1411	31.8	4.2	537	5	BX568099	BX568099	BX568099


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ORIGIN
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Best Local Similarity 99.3%; Pred. No. 2.1e-201;
Matches 750; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 7 AGCGTTTCTGAGCCAGGGGTGACCATGACCTGCTGCGAAGATGGACATCCTGCAATGGA 66
Db 2 AACGTTTCTGAGCCAGAGGTGACCATGACCTGCTGCGAAGATGGACATCCTGCAATGGA 61

QY 67 TTCAGCCTGCTGTTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATACCTTAATTGTC 126
Db 62 TTCAGCCTGCTGTTCTACTGCTGTTAGGAGTAGTTCTCAATGTGATACCTTAATTGTC 121

QY 127 AGCTTAGTTGAGGAAGACCAATTTTCTCAAAACCCCATCTCTTGCTTTGAGTGGTGGTTC 186
Db 122 AGCTTAGTTGAGGAAGACCAATTTTCTCAAAACCCCATCTCTTGCTTTGAGTGGTGGTTC 181

QY 187 CCAGGAATTATAGGAGCAGGTCTGATGGCCATTCCAGCAACAACAATGTCCTTGACAGCA 246
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QY 247 AGAAAAAGAGCGTCTGCAACAACAGAACTGGAATGTTTCTTTCATCATATTTTTCAGTGTG 306
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QY 367 CCTCTCATGTGTAATTCTCCAGCAACAGTAATGCCAATTGTGAATTTTCATTGAAAAAC 426
Db 362 CCTCTCATGTGTAATTCTCCAGCAACAGTAATGCCAATTGTGAATTTTCATTGAAAAAC 421

QY 427 ATCAGTGACATTCCAGAAATCCTTCAACTGTCAGTGGTGTTCATATGACTCTTGTGCA 486
Db 422 ATCAGTGACATTCCAGAAATCCTTCAACTGTCAGTGGTGTTCATATGACTCTTGTGCA 481

QY 487 CCTCCTACTGTTTCAATAAACCACCAAGTAACGACACCAATGGCGAGTGGCTGGAGAGCA 546
Db 482 CCTCCTACTGTTTCAATAAACCACCAAGTAACGACACCAATGGCGAGTGGCTGGAGAGCA 541

QY 547 TCTAGTTTCCACTTCGATTCTGAAGAAAAACAACATAGGCTTATCCACTTCTCAGTATTT 606
Db 542 TCTAGTTTCCACTTCGATTCTGAAGAAAAACAACATAGGCTTATCCACTTCTCAGTATTT 601

QY 607 TTAGGTCATTGCTTGTGGAAATCTGGAGTCTGTTGGGCTCAGTCAGATAGTCAATC 666
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QY 667 GGTTTCCTTGGCTGTCTGTGTGGAGTCTCTAAGCGAAGAGTCAAATTTGTGTAGTTTAAT 726
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QY 727 GGGAAATAAAATGFAAGTATCAGTAGTTTGAATAAA 761
Db 722 GGGAAATAAAATGFAAGTATCAGTAGTTTGAATTA 756

RESULT 2
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LOCUS BM923919
DEFINITION AGENCOURT_6709870 NIH_MGC_116 Homo sapiens cdna clone IMAGE:5760060
5', mRNA Sequence.
ACCESSION BM923919
VERSION BM923919.1 GI:19374298
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 995)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cdna Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12806 row: h column: 13
High quality sequence stop: 687.

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pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."

ORIGIN
Query Match      96.1%; Score 736; DB 4; Length 995;
Best Local Similarity 99.2%; Pred. No. 2.3e-198;
Matches 750; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 7 AGCGTTTCTGAGCCAGGGGTGACCATGACCTGCTGCGAAGATGGACATCCTGCAATGGA 66
Db 1 AACGTTTCTGAGCCAGAGGTGACCATGACCTGCTGCGAAGATGGACATCCTGCAATGGA 60

QY 67 TTCAGCCTGCTGTTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATACCTCTAATTGTC 126
Db 61 TTCAGCCTGCTGTTCTACTGCTGTTAGGAGTAGTTCTCAATGTGATACCTCTAATTGTC 120

QY 127 AGCTTAGTTGAGGAAGACCAATTTTCTCAAAACCCCATCTCTTGTGTTGAGTGGTGGTTC 186
Db 121 AGCTTAGTTGAGGAAGACCAATTTTCTCAAAACCCCATCTCTTGTGTTGAGTGGTGGTTC 180

QY 187 CCAGGAATTATAGGAGCAGGTCTGATGGCCATTCCAGCAACAACAATGTCTCTTGACAGCA 246
Db 181 CCAGGAATTATAGGAGCAGGTCTGATGGCCATTCCAGCAACAACAATGTCTCTTGACAGCA 240

QY 247 AGAAAAAGAGCGTCTGCAACAACAGAACTGGAATGTTTCTTTCATCATATTTTTCAGTGTG 306
Db 241 AGAAAAAGAGCGTCTGCAACAACAGAACTGGAATGTTTCTTTCATCATATTTTTCAGTGTG 300

QY 307 ATCAGAGTCATTGGTGCTCTGTATTGCATGCTGATATCCATCCAGGCTCTCTTAAAGGT 366
Db 301 ATCAGAGTCATTGGTGCTCTGTATTGCATGCTGATATCCATCCAGGCTCTCTTAAAGGT 360

QY 367 CCTCTCATGTGTAATTCTCCAGCAACAGTAATGCCAATTTGTGAATTTTTCATTGAAAAAC 426
Db 361 CCTCTCATGTGTAATTCTCCAGCAACAGTAATGCCAATTTGTGAATTTTTCATTGAAAAAC 420

QY 427 ATCAGTGACATTCCAGAAATCCTTCAACTGTCAGTGGTGTTCATATGACTCTTGTGCA 486
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QY 603 ATTTTGTAGGCTATTTGCTTGTGGAATCTGGAGGTCCTGTTGGGCTCAGTCAGATAGT 662
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QY 663 CATCGGTTTCCCTTGGCTGCTCTGTGGAGTCTCTAAGCGAAGAAGTCAAAATTTGTAGTT 722
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RESULT 7
CO582384 896 bp mRNA linear EST 20-JUL-2004
LOCUS ILLUMIGEN MCQ_45837 Katze MMJJ Macaca mulatta cDNA clone
DEFINITION IBIUW:19176 5' similar to Bases 2 to 835 highly similar to human
FLJ22800 (Hs.156652), mRNA sequence.

ACCESSION CO582384
VERSION CO582384.1 GI:50414146
KEYWORDS EST.

SOURCE Macaca mulatta (rhesus monkey)
ORGANISM Macaca mulatta

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.

REFERENCE 1 (bases 1 to 896)
AUTHORS Katze,M.G., Thomas,M., Korth,M., Iadonato,S.P. and Magness,C.L.
TITLE Large-scale Rhesus Macaque cDNA Sequencing
JOURNAL Unpublished (2003)
COMMENT Contact: C. Magness

Illumigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
Tel: 2063780400
Fax: 2063780408

Email: cmagness@illumigen.com
Sequenced on 2004.06.22. 521 Q20 bases. Library Preparation: Prof.
Michael Katze Lab at University of Washington DNA Sequencing:
Illumigen Biosciences Inc. For further information, see
http://www.macaque.org

PCR Primers
FORWARD: CCTCACTAAAGGGAACAAA
BACKWARD: CACTATAGGCGGAATTGGTA
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POLYA=No.

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Site 2: BsrG I; Created from CloneMiner cDNA Library
Construction kit (catalog #18249-029)"

ORIGIN

Query Match 79.7%; Score 610.2; DB 7; Length 896;
Best Local Similarity 91.1%; Pred. No. 1.7e-162;
Matches 648; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

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Db 2 TGGCCATGACCTGCTGCGAGGGATGGACATCCTGCAATGGATTACGCCCTGCTGTTCTAC 61
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QY 86 TGCTGTAGGAGTAGTTCTCAATGGGATACCTCTAATTGTCAGTTAGTTGAGGAAGACC 145

Db 62 TGCTGTAGGAGTAGTTCTCAATGCGATGCCTCTAATTGTCAAGTTAATTGAGGAAGACC 121
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QY 146 AATTTTCTCAAAACCCCATCTCTTGGCTTTGAGTGGTGGTCCCAGGAATTATAGGAGCAG 205
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Db 122 GATCTTCTCAAAACCCCATCTCTTGGCTTTGAGTGGTGGTCCCAGGAATTATAGGAGCAG 181
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QY 206 GTCTGATGGCCATTCCAGCAACAACAATGTCTTGCAGCAGCAAGAAAAAGCGTCTGCA 265
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Db 182 GTCTGATGGCCATTCCAGCAACAACAATGTCTTGCAGCAGCAAGAAAAAGAAATGCTGCA 241
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QY 266 ACAACAGAACTGGAAATGTTTCTTTTCATCATTTTTTCAGTGTGATCACAGTCATTGGTGCTC 325
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Db 242 ACAACAGAACTGGAAATGTTTCTTTTCATCATTTTTTCAGTGTGATCACAGTCATTGGTGCTC 301
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QY 326 TGTATTGCATGCTGATATCCATCCAGGCTCTCTTAAAGGTCCTCTCATGTGTAATTCTC 385
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QY 386 CAAGCAACAGTAATGCCAATTGTGAATTTTCATTGAAAAACATCAGTGACATTCATCCAG 445
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Db 362 AAGGCAACAGTACTGCCAATTGTGAATTTTCATTGAAAAACATCTGTGACATTCGCCCGG 421
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QY 446 AATCCTTCAACTTGCAGTGGTTTTTTCATGACTCTTGTGCACCTCCTACTGGTTTCAATA 505
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Db 422 AAGACTTCAACTTGCAGTGGTTTTTTCATGACTCTTGTGTCCTCCGCTGGCTCCAAAA 481
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QY 506 AACCCACAGTAACGACACCATGGGAGTGGCTGGAGAGCATCTAGTTTCCACTTCGATT 565
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Db 602 GAATTCGGAGGTCCTGTTGGGCTCAACCAATAGCCATTGGTTCCCTTGGTGTCTGT 661
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QY 686 GTGGAGTCTCTAAGCGAAGAAGTCAAAATGTGTAGTTTAATGGGAATAAAA 736
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Db 662 GTGGAGTCTCTAAGCAAGAAATCAAAATGTGGTATTTTAATGGGAATAAA 712
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RESULT 8

CO582384

LOCUS

DEFINITION

sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Bos taurus (cow)

Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

Bovinae; Bos.

REFERENCE 1 (bases 1 to 713)

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Richard G. Baumann

Bovine Functional Genomics Lab

ANRI

BLDG 162; BARC-EAST, Beltsville, MD 20705, USA

Tel: 3015048604

Fax: 3015048744

Email: rbaumann@anri.barc.usda.gov

Single pass sequencing. Bases called and trimmed with phred
0.000925 using options -trim_alt -' -trim_fasta. Vector identified
by cross_match using options -minmatch 12 -minscore 18

CN793461 713 bp mRNA linear EST 26-MAY-2004
4128489 BARC 8BOV Bos taurus cDNA clone 8BOV_48115 5', mRNA

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	/clone="8BOV 48I15"
	/sex="Female"
	/tissue_type="Epithelial, Muscle"
	/dev_stage="Lactating, Neonatal"
source	/clone_lib="BARC 8BOV"
	/note="Organ: Intestine; Vector: pCMVSPORT6.1; Site 1:
	NotI; Site 2: EcoRI; Normalized cow cDNA intestinal
	library in pCMVSPORT6.1, constructed from equimolar mRNA
	pools derived from 5 sources, 4 lactating intestinal, 1
	neonatal intestinal 4/5 Lactating, Proximal Duodenum,
	Jejunum, Distal Ileum, Colon, 1/5 Neonatal, Proximal
	Duodenum, Jejunum, Distal Ileum"
ORIGIN	
Query Match 64.8%; Score 496; DB 7; Length 713;	
Best Local Similarity 82.0%; Pred. No. 5.7e-130;	
Matches 584; Conservative 0; Mismatches 125; Indels 3; Gaps 1;	
QY	14 CTGAGCAGGGGTGACCATGACCTGCTGGGAAGGATGACATCCTGCAATGGATTGAGCC 73
Db	
QY	74 TGCTGGTTCTACTGCTGTAGGAGTAGTTCTCAATGCGATACCTCTAATTGTCAGCTTAG 133
Db	
QY	62 TGCTGGTTCTGCTTCTGTTGGGAGTAACCTCAACGCAATACCTCTAATTTTAAACTTTG 121
Db	
QY	134 TTGAGGAAGACCAATTTTCTCAAAACCCCATCTCTTGCTTTGAGTGGTGTCCAGGAA 193
Db	
QY	122 TGGATGAAGACCAATTTTGTGAAACCCCATCTCCTGCTTTGAATGGTGTCCCTGGAA 181
Db	
QY	194 TTATAGGAGCAGGTCTGATGGCCATTCCAGCAACAACAATGTCTTGACAGCAAGAAAA 253
Db	
QY	182 TTATTGAGCAGGTGTGATGGCGATTCCAGCAACAACGATGTCTTGGCAGCGAGGAAA 241
Db	
QY	254 GAGCGTGTGCAACAACAGAACTGGAATGTTCTTTTCATCATTTTTCAGTGTGATCACAG 313
Db	
QY	242 GAGCGTGTGCAACAACAACCGGATGTTCTTTTCATCATCTTCTGAACGCCATCACAG 301
Db	
QY	314 TCATTGTTGCTCTGTATTGTCATGCTGATATCCATCCAGGCTCTCTTAAAAGGTCCTCTCA 373
Db	
QY	302 TCATTGAGCTGCGTATTGCTGCTGCTGCTCCATCCAGGCTCTCGCGAGGGCCCTCTCA 361
Db	
QY	374 TGTGTAATTTCTCCAAGCAACAGTAATGCCAATTGTGTAATTTTCATTGAAAAACATCAGTG 433
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QY	362 TTTGCAACTCTCAAAGCAACACAACTTCCAGTTGTGTAATTTTCCCTTAAAAACTTAACTG 421
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QY	434 ACATTCAATCCAGAAATCCTTCAACTTGCAGTGGTTTTTCAATGACTCTTGTGCACCTCCTA 493
Db	
QY	422 CCAATTATAAAGAATCCTTTGATCTGCAAGTGGTCTTCGAAGACTCTTGTGTTCCCTCATA 481
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QY	494 CTGGTTTCAATAAACCCACCAGTAACGACACCATTGGCGAGTGGCTGGAGAGCATCTAGTT 553
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QY	482 CGGATTTCCAATAATCCCTCCATCACCACACAAAGCCAAATAACTGGAGAGTATACAACT 541
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Db	
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QY	614 TATTGCTTGTGGAAATCTGGAGGTCTGTTTGGGCTCAGTCAGATAGTCATCGGTTTCC 673
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QY	602 TACTGCTTGTGGCAATTTCTCGAGATTTCTGTTTGGACTCAGTCAGATAATCATCGGCTTCT 661
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QY	674 TTGGCTGTCTGTGT ---GGAGTCTCTAAGCGAAGAGTCAAAATTGTGTAGTT 722

Db	
	662 TTGGCTGTCTGTGTGGAGAGTCTCTAACGGAAGAACCAATCGTGTAGTT 713
RESULT 9	
COS80240	
LOCUS	
DEFINITION	
ILLUMIGEN MCQ_48946 Katze_MMDD Macaca mulatta cDNA clone	
IBIUW:18267 5' similar to Bases 212 to 788 highly similar to human	
FLJ22800 (Hs.156652), mRNA sequence.	
COS80240	
COS80240.1 GI:50411340	
EST.	
SOURCE	
Macaca mulatta (rhesus monkey)	
ORGANISM	
Macaca mulatta	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;	
Cercopitheciinae; Macaca.	
1 (bases 1 to 888)	
REFERENCE	
KATZE, M.G., THOMAS, M., KORTH, M., IADONATO, S.P. and MAGNESS, C.L.	
TITLE	
Large-scale Rhesus Macaque cDNA Sequencing	
JOURNAL	
Unpublished (2003)	
COMMENT	
Contact: C. Magness	
Illumigen Biosciences Inc.	
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA	
Tel: 2063780400	
Fax: 2063780408	
Email: cmagness@illumigen.com	
Sequenced on 2004.07.02. 622 Q20 bases. Library Preparation: Prof.	
Michael Katze Lab at University of Washington DNA Sequencing:	
Illumigen Biosciences Inc. For further information, see	
http://www.macaque.org	
PCR Primers	
FORWARD: CCCTCACTAAAGGGAACAAAA	
BACKWARD: CACTATAGGCGGAATTGGGTA	
Insert Length: 888 Std Error: 0.00	
Plate: CL000405 row: F column: 11	
Seq primer: CCCTCACTAAAGGGAACAAAA	
POLYA=Yes.	
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Location/Qualifiers	
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/sex="male"	
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/lab_host="Electromax DH10B"	
/clone_lib="Katze_MMDD"	
/note="Organ: duodenum; Vector: pDONR 222; Site 1: BsrG I;	
Site 2: BsrG I; Created from CloneMiner cDNA Library	
Construction kit (catalog #18249-029)"	
ORIGIN	
Query Match 64.4%; Score 493.6; DB 7; Length 888;	
Best Local Similarity 84.5%; Pred. No. 3e-129;	
Matches 607; Conservative 0; Mismatches 44; Indels 67; Gaps 2;	
QY	20 CAGGGGTGACCATGACCTGCTGCGAAGGATGGACATCCTGCAATGGATTGAGCTGCTGG 79
Db	
QY	18 CCGGGGTGACCATGACCTGCTGCGAGGGATGGACATCCTGCAATGGATTGAGCTGCTGG 77
Db	
QY	80 TTCTACTGCTGTAGGAGTAGTTCTCAATGCGATACCTCTAATTGTCAGCTTAGTTGAGG 139
Db	
QY	78 TTCTACTGCTGTAGGAGTAGTTCTCAATGCGATGCTCTAATTGTCAGCTTAATTGAGG 137
Db	
QY	140 AAGACCAATTTTCTCAAAACCCCATCTCTTTGAGTGGTGTCCAGGAATTATAG 199
Db	
QY	138 AAGACCGATCTTCTCAAAACCCCATCTCTTTGAGTGGTGTCCAGGAATTATAG 197
Db	
QY	200 GAGCAGGTCTGATGSCCATTTCCAGCAACAACAATGTCCTTGACAGCAAGAAAAAGGCT 259
Db	

Db 198 GAGCAGGCTCTGATG----- 211

QY 260 GCTGCAACAACAGAACTGGAATGTTTCTTTTCATCATTTTTCAGTGTGATCACAGTCATTG 319

Db 212 -----ATGTTTCTTTTCATCACTTTTCAGTGTAAATCACAGTCATTG 251

QY 320 GTGCTCTGTATTGCTGATATCCATCCAGGCTCTCTTAAAGGTCCTCTCATGTGTA 379

Db 252 GTGCTCTGTATTGCTGATATCCATCCAGGCTCTCTTAAAGGTCCTCTCATGTGTA 311

QY 380 ATTCTCCAAGCAACAGTAATGCCAATTGTGAATTTTCATTGAAAAACATCAGTGACATT 439

Db 312 ATTCTCAAGGCAACAGTACTGCCAATTGTGAATTTTCATTGAAAAACATCAGTGACATT 371

QY 440 ATCCAGAATCCTTCAACTTGCAGTGGTTTTTCAATGACTCTTGTGCACCTCCTACTGGTT 499

Db 372 GCCCGGAAGACTTCAACTTGGGTGGTTTTTCAATGACTCTTGTGTGCCTCCGCTGGCT 431

QY 500 TCAATAAACCCACCAGTAACGACACCATGGCGAGTGGCTGGAGAGCATCTAGTTCCACT 559

Db 432 CCAAAAACCCACCAGCAATGACGTACCGGCCAGCGGCTGGAGAGCATCTAGTCTGCACT 491

QY 560 TCGATTCTGAAGAAAAACAACATAGGCTTATCCACTTCTCAGTATTTTATAGTCTA-TTG 618

Db 492 TCAATTCTGAAGAAAAACAACACAGGCTATCCACTTCTCAGTCTTTTATAGTCTATTG 551

QY 619 CTGTTTGGAAATCTGGAGGTCCTGTTTGGGCTCAGTCAGATAGTCATCGGTTTCCTTGGC 678

Db 552 CTGTGGGAATTTGGAGGTCCTGTTCCGGCTCAGTCAGATAGTCATCGGTTTCCTTGGC 611

QY 679 TGTCTGTGTGGAGTCTCTAAGCGAAGAAGTCAAAATGTGTAGTTTAAATGGAATAAAA 736

Db 612 TGTCTGTGTGGAGTCTCTAAGCGAAGAAGTCAAAATGTGTAGTTTAAATGGAATAAAA 669

RESULT 10

CN786443

LOCUS

DEFINITION

4120438 BARC 8BOV Bos taurus cDNA clone 8BOV_29K17 5', mRNA

sequence.

CN786443

VERSION

KEYWORDS

SOURCE

ORGANISM

Bos taurus (cow)

Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

1 (bases 1 to 705)

Baumann,R.G., Baldwin,R.L., Sonstegard,T.S., Van Tassell,C.P. and Matukumalli,L.K.

Construction and Analysis of a cDNA Library Generated From Intestinal Muscle and Epithelial Tissues of Holstein Cattle Unpublished (2004)

Contact: Richard G. Baumann

Bovine Functional Genomics Lab

ANRI

BLDG 162: BARC-EAST, Beltsville, MD 20705, USA

Tel: 3015048604

Fax: 3015048744

Email: rbaumann@anri.barc.usda.gov

Single-pass sequencing. Bases called and trimmed with phred 0.000925 using options -trim_alt ',' -trim_fasta. Vector identified by cross_match using options -minmatch 12 -minscore 18

Plate: 29 row: K column: 17

Seq primer: CCTATTAGGTGACACTATAGAAC

High quality sequence stop: 705.

FEATURES

source

1. .705

/organism="Bos taurus"

/mol_type="mRNA"

/strain="Holstein"

/db_xref="taxon:9913"

/clone="8BOV_29K17"

/sex="Female"

/tissue_type="Epithelial, Muscle"

/dev_stage="Lactating, Neonatal"

/lab_host="DH10B Tona"

/clone_lib="BARC 8BOV"

/note="Organ: Intestine; Vector: pCMVSPORT6.1; Site 1: NotI; Site 2: EcoRI; Normalized cow cDNA intestinal library in pCMVSPORT6.1, constructed from equimolar mRNA pools derived from 5 sources, 4 lactating intestinal, 1 neonatal intestinal 4/5 Lactating, Proximal Duodenum, Jejunum, Distal Ileum, Colon, 1/5 Neonatal, Proximal Duodenum, Jejunum, Distal Ileum"

ORIGIN

Query Match 64.3%; Score 492.2; DB 7; Length 705;

Best Local Similarity 82.1%; Pred. No. 6.9e-129;

Matches 579; Conservative 0; Mismatches 123; Indels 3; Gaps 1;

QY 34 ACCTGCTGCGAAGGATGGACATCCTGCAATGGATTTCAGCCTGCTGGTTCCTACTGCTGTTA 93

Db 1 ACCTGCTGCGAAGGATGGACATCCTGCAATGGATTTCAGCCTGCTGGTTCCTGCTGCTGTG 60

QY 94 GGAGTAGTTCTCAATGGGATACCTCTAATTGTTCAGCTTAGTTGAGGAAGACCAATTTTCT 153

Db 61 GGAGTAACCTCTCAACGCAATACCTCTAATTTTAACTTTTGGGATGAAGACCAATTTT 120

QY 154 CAAAACCCCATCTCTTGGCTTTGAGTGGTGGTTCCCAGGAATTATAGGAGCAGTCTGATG 213

Db 121 GAAAACCCCATCTCTTGGCTTTGAATGGTGGTCCCTGGAATTATTTGGAGCAGTGTGATG 180

QY 214 GCCATTCCAGCAACAACAATGTCTTGACAGCAAGAAAAGAGCGTGTGCAACAACAGA 273

Db 181 GCGATTCCAGCAACAACGATGTCTTGGCAGCGGAGAAAAGAGCATGTCTGCAACAACAA 240

QY 274 ACTGGAATGTTTCTTTTCATCATTTTTCAGTGTGATCAGATGATTCATCCAGAATCCTTC 333

Db 241 ACCGGGATGTTTCTTTTCATCATCTTCTGAAAGCCATCAGATCATTTGGAGCTGGTATTC 300

QY 334 ATGCTGATATCCATCCAGGCTCTCTTAAAGGTCCTCTCATGTGTAATTTCTCAAGCAAC 393

Db 301 CTGCTGGTGTCCATCCAGGCTCTCGCGGAGGGCCCTCTCATTTGCAACTCTCAAGCAAC 360

QY 394 AGTAATGCCAATTTGTGAATTTTTCATTGAAAAACATCAGTGACATTCATCCAGAATCCTTC 453

Db 361 ACAACTCCAGTTGTGAATTTTCCCTTAAAAAATTAACTGCAATTTATAAAGAAATCCTTT 420

QY 454 AACTTGCAGTGGTTTTCATGACTCTTGTGCACTTCTGTCACCTCTCTACTGGTTTCAATAAACCACC 513

Db 421 GATCTGAGTGGTTCTTGAAGACTCTTGTGTTCTCTATACGGATTCCTCAATTAATCCCTCC 480

QY 514 AGTAACGACACCATGGCGAGTGGCTGGAGAGCATCTAGTTTCCACTTCGATTTCTGAAGAA 573

Db 481 ATCCACAACACAACAGCCAATAACTGGAGAGTATACAACTTGCACTTCAATTTCTATAGAA 540

QY 574 AACAAACATAGGCTTATCCACTTCTCAGTATTTTATAGTCTATTGCTTGTGGAATTTCTG 633

Db 541 AACCAACACAGGATTTATCCATTTCTCAGTATTTTATAGTCTACTGCTTGTGGGCAATTTCTC 600

QY 634 GAGGTCCTGTTTGGGCTCAGTCAGATAGTCATCGGTTTTCCTTGGCTGTCTGTGT---GGA 690

Db 601 GAGATTCTGTTTGGACTCAGTCAGATAATCATCGGCTTCTTTGGCTGTCTGTGTGGGAGGA 660

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Db 661 GTCTCTAAGCGAAGAGCAAAATCGTGTAGTTTGTAGTAACAATAAA 705

RESULT 11

CN837742

LOCUS

DEFINITION

4062718 BARC 8BOV Bos taurus cDNA clone 8BOV_15H12 5', mRNA

sequence.

CK837742

726 bp

mRNA

linear

EST 04-MAR-2004

QY	623	TTGGAATTCTGGAGGTCCTGTTTGGGCTCAGTCAGATAGTCATCGGTTTCCTTGGCTGTC	682
Db	624	TTGGAATCCTGGAGCTCCTGTTTGGGCTCAGTCAGATACCTATGTTCTCTTGGCTGTC	683
QY	683	TGTTGGAGTCTCTAAGCGAAGAGTCAAAATGTGTAGTTTAATGGGATAAAAAATGTAAG	742
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QY	743	TATCAGTAGTTTGAAAAA	760
Db	739	TATCAGTACTTTGAATAA	756
RESULT 14			
BY707590			
LOCUS			
DEFINITION	BY707590 RIKEN full-length enriched, 10 day old male pancreas Mus	972 bp	EST 16-DEC-2002
ACCESSION	musculus cDNA clone 1810018L02 5', mRNA sequence.		
VERSION	BY707590		
KEYWORDS	BY707590.1 GI:27118767		
SOURCE	EST.		
ORGANISM	Mus musculus (house mouse)		
REFERENCE	Mus musculus		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 972)		
	Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaïdo, I., Oeato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Shomobach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Brusic, V., Chothia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A., Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A., Kawaji, H., Kawasaki, Y., Kedzierski, R. M., King, B. L., Konagaya, A., Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W. J., Perte, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C. A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L. G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S., Rogers, J., Birney, E. and Hayashizaki, Y.		
TITLE	Analysis of the mouse transcriptome based on functional annotation		
JOURNAL	of 60,770 full-length cDNAs		
MEDLINE	Nature 420, 563-573 (2002)		
PUBMED	22354683		
COMMENT	12466851		
	Contact: Yoshihide Hayashizaki		
	Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute		
	The Institute of Physical and Chemical Research (RIKEN)		
	1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan		
	Tel: 81-45-503-9222		
	Fax: 81-45-503-9216		
	Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/		
	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Saito, R., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Takeda, Y., Waki, K., Watanabe, A., Muramatsu, M. and Hayashizaki, Y.		
Direct Submission			
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)			
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)			
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)			
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)			
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.			
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.			
FEATURES	Location/Qualifiers		
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	/dev_stage="10 day old"		
	/clone_lib="RIKEN full-length enriched, 10 day old male pancreas"		
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Query Match	61.9%;	Score 473.8;	DB 6; Length 972;
Best Local Similarity	80.8%;	Pred. No. 1.3e-123;	
Matches	594;	Conservative 0;	Mismatches 127; Indels 14; Gaps 3;
Qy	23	GGGTGACCATGACCTGCTGCGAAGGATGGACATCCTGCAATGGATTTCAGCCTGCTGGTTC	82
Db	29	GGAAACCATGACGCTGCTGTGAAGGGTGGACATCCTGCAATGGCTTCAGCCTGCTCATTC	88
Qy	83	TACTGCTGTTAGGAGTAGTTCTCAATGGCATACCTCTAAATGTGTCAGCTTAGTGAGGAAG	142
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Qy	143	ACCAATTTTCTCAAAACCCCATCTCTTGTGTTGAGTGGTGTCCAGGAATTATAGGAG	202
Db	149	ACTCGACTTCTCAAAACCCCATCTCTGCTATGAGTGGTGGTTTCCAGGAATTATAGGAG	208
Qy	203	CAGGTCTGATGGCCATTCCAGCAACAACAAATGTCTTTCAGCAAGAAAAAGCGTGTCT	262
Db	209	CAGGTCTGATGGCCATCCAGCAACAACAAATGTCTTTCAGCAAGAAAAAGCGTGTCT	268
Qy	263	GCAACAACAGAACTGGAATGTTTCTTTCATCATTTTTCAGTGTGATCACAGTCAATGGTG	322
Db	269	GCAACAACAGAACTGGAATGTTTCTTTCATCATTTTTCAGTGTGATCACAGTGTGGTG	328
Qy	323	CTCTGTATTGCATGCTGATATCCATCCAGGCTCTCTTAAAGGTCCTCTCATGTGTAATT	382
Db	329	CTGTGTATTGCATGTTGGTATCACTCCAGGCTCTCTTGGAGGACCTCTAAATTTGTAATA	388
Qy	383	CTCCAAGCAACAGTAATGCCAATTGTGAATTTTCATTGAAAAACATCAGTGACATTCATC	442
Db	389	CTCAGGCCAACAGTACTGTCACTTGTGAATTTTCATTGAAAAACCTTAAGTAAATTTGATC	448
Qy	443	CAGAATCCTTCAACTTGCAGTGGTGTTCATCAATGACTCTTGTGCACTCTCTACTGTTTCA	502
Db	449	CTGAATCCTTCAATCTGCTGTGGTTCCTCAATGGCAGTCTGTGTCTCTACTGATTTTA	508
Qy	503	ATAAACCACCAAGTAACGACACCATGGCAGTGGCTGGAGAGCATCTAGTTTCCACTTCG	562
Db	509	AAAACCCCAACC---ATCAATAACATGGTCAGTAACCTGGAAAAATACC-----CAACTCCA	559

QY	563	ATTCTGAAGAAACAACATAGGCTTATCCACTTCTCAGTATATTTTAGGTCATTGCTTG	622		
Db	560	ACTCTGAAGAAGACAGACACAGGATTTTCCACTTCTCAGTATTTATGAGTCTCCTGCTTG	619		
QY	623	TTGGAATTCTGGAGGTCTGTGTTGGGCTCAGTCAGATAGTCATCGGTTTCCTTGGCTGTC	682		
Db	620	TTGGAATCCTGGAGCTCTGTGTTGGGCTCAGTCAGATACTCATTTGGTTTCCTTGGCTGTC	679		
QY	683	TGTGTGGAGTCTCTAAGCGAAGAGTCAAATTTGTGTAGTTTAAATGGGAATAAAATGTAAG	742		
Db	680	TGTGTGGCGTCTCTCAGCGACGGAGTCAAATT-----GTATAAAGGGCAATATACTAGAA	734		
QY	743	TATCAGTAGTTTGAA	757		
Db	735	TATCAGTACTTTGAA	749		
RESULT 15					
AK017154					
LOCUS	AK017154	796 bp	mRNA linear HTC 03-APR-2004		
DEFINITION	Mus musculus 11 days pregnant adult female ovary and uterus cDNA, RIKEN full-length enriched library, clone:5033405M13				
	product:similar to CDNA: FLJ22800 FIS, CLONE KAI2630 [Homo sapiens], full insert sequence.				
ACCESSION	AK017154				
VERSION	AK017154.1	GI:12856263			
KEYWORDS	HTC; CAP trapper.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	1				
AUTHORS	Carninci, P. and Hayashizaki, Y.				
TITLE	High-efficiency full-length cDNA cloning				
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)				
MEDLINE	99279253				
PUBMED	10349636				
REFERENCE	2				
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.				
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes				
JOURNAL	Genome Res. 10 (10), 1617-1630	(2000)			
MEDLINE	20499374				
PUBMED	11042159				
REFERENCE	3				
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.				
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer				
JOURNAL	Genome Res. 10 (11), 1757-1771	(2000)			
MEDLINE	20530913				
PUBMED	11076861				
REFERENCE	4				
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.				
TITLE	Functional annotation of a full-length mouse cDNA collection				
JOURNAL	Nature 409, 685-690	(2001)			
REFERENCE	5				
AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.				
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs				
JOURNAL	Nature 420, 563-573	(2002)			
REFERENCE	6				
AUTHORS	(bases 1 to 796)				
	Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K.,				

TITLE		JOURNAL	
Hiraoka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.			
Direct Submission			
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)			
Please visit our web site (http://genome.gsc.riken.jp/) for further details.			
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTT 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. cDNA of size comprised longer than 7 kb was selected before cloning. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI. Host: DH10B.			
FEATURES		Location/Qualifiers	
source		1..796	
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		/tissue_type="ovary and uterus"	
		/clone_lib="RIKEN full-length enriched mouse cDNA library"	
		/dev_stage="11 days pregnant adult"	
CDS		42..722	
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/protein_id="BAB30618.1"			
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ORIGIN			
Query Match 61.8%; Score 473.6; DB 3; Length 796;			
Best Local Similarity 80.6%; Pred. No. 1.4e-123;			
Matches 595; Conservative 0; Mismatches 129; Indels 14; Gaps 3;			
QY	23	GGGTGACCATGACCTGCTGCGAAGGATGGACATCTCGCAATGGATTGAGCTGCTGTTTC	82
Db	34	GGAATAACCATGACGTGCTGTGAAGGGTGGACATCTCGCAATGGCTTCAGCTCATTC	93
QY	83	TACTGCTGTAGGAGTAGTTCTCAATGCGGATACCTCTAATTGTCAGCTTAGTTGAGGAAG	142
Db	94	TGATCCTGCTAGGAGTGGTTATCAATTGTATACCCCTGGGAATCAGCTTAGTGGAGGCAG	153

Qy	143	ACCAATTTTCTCAAAACCCCATCTCTTGCTTTGAGTGGTGGTTCCAGGAATTATAGGAG	202
Db	154	ACTCGACTTCTCAAAACCCCATCTCTGCTATGAGTGGTGGTTCCAGGAATTATAGGAG	213
Qy	203	CAGGTCGTGATGGCCATTCCAGCAACAATGTCTTGACAGCAAGAAAAAGAGCGTGCT	262
Db	214	CAGGTCGTGATGGCCATCCAGCAACAATGTCTTGACAGCAAGAAAAAGAGCGTGCG	273
Qy	263	GCAACAACAGAACTGGAATGTTCTTTTCATCATTTTTCAGTGTGATCACAGTCATTGGTG	322
Db	274	GCAACAATAAGACTGGGATGTTCTTTTCATCACTCTTCAGTGTGATCACAGTGTGGTG	333
Qy	323	CTCTGTATTGCATGTGATATCCATCCAGGCTCTCTTAAAGTCTCTCTCATGTGTAATT	382
Db	334	CTGTGTATTGCATGTGGTATCACTCCAGGCTCTCTTGAAGACCTCTAATTGTATA	393
Qy	383	CTCCAAGCAACAGTAATGCCAATTGTGAATTTTCATTGAAAAACATCAGTGACATTATC	442
Db	394	CTCAGGCCAACAGTACTGTCACTTGTGAATTTTCATTGAAAAACTTAAGTAAATTTGATC	453
Qy	443	CAGATCCTTCAACTGCAGTGGTCTTCAATGACTCTTGTCGACCTCTCTACTGGTTTCA	502
Db	454	CTGAATCCTTCAATCTGCTGTGGTCTTCAATGGCACTTGTTCTCTCTACTGATTTTA	513
Qy	503	ATAAACCCACCAGTAAACGACACCATGGCGAGTGGCTGGAGAGCATCTAGTTTCCACTTCG	562
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Qy	563	ATTCTGAAGAAAAACAACATAGGCTTATCCACTCTCAGTATTTTTAGGTCTATTGCTTG	622
Db	565	ACTCTGAAGAAGACAGACACAGGATTTTCCACTCTCAGTATTTATGAGTCTCCTGCTTG	624
Qy	623	TTGGAATTCTGGAGTCTGTTTGGGCTCAGTCAGATAGTCATCGGTTTCCTTGGCTGTC	682
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Qy	683	TGTGTGGAGTCTCTAAGCGAAGAGTCAAAATGTGTAGTTTAAATGGGAATAAAAATGTAAG	742
Db	685	TGTGTGGCGTCTCTCAGCGACGGAGTCAAAAT-----GTATAAAGGGCAATAAACTAGAA	739
Qy	743	TATCAGTAGTTTGAATAA	760
Db	740	TATCAGTACTTTGAATAA	757